

SEQUENCE LISTING

<110> Tavtigian, Sean V.
 Teng, David H.F.
 Simard, Jacques
 Rommens, Johanna M.
 Myriad Genetics, Inc.

<120> Chromosome 17p-Linked Prostate Cancer Susceptibility
 Gene and a Paralog and Orthologous Genes

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<150> US 60/107,468
<151> 1998-11-06

<150> 09/434,382
<151> 1999-11-05

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<170> PatentIn Ver. 2.0

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 Thr Met Thr Val Tyr Gln Ile Pro Ile His Ser Glu Gln Arg Arg Gly
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卷之三

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Met Trp
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gcg ctc cgc tca ctg ttg cgt ccc ctt ggc ctg cgc acc atg tcg cag 104
 Ala Leu Arg Ser Leu Leu Arg Pro Leu Gly Leu Arg Thr Met Ser Gln
 5 10 15

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ggc tcg gct cgt cgg ccg cgg cca ccc aag gac cca ctg cga cac ctg 152
Gly Ser Ala Arg Arg Pro Arg Pro Pro Lys Asp Pro Leu Arg His Leu
 20          25          30

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cgt acg ccg gag aag cgc ggc ccg ggt ccc ggg ggc ccg aac acc acc gtg 200
Arg Thr Arg Glu Lys Arg Gly Pro Gly Pro Gly Gly Pro Asn Thr Val
35          40           45           50

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tac	ctg	cag	gtg	gtg	gct	gct	ggc	ggc	cg	gac	gct	ggg	gct	gct	ctc	248
Tyr	Leu	Gln	Val	Val	Ala	Ala	Gly	Gly	Arg	Asp	Ala	Gly	Ala	Ala	Leu	.
					55				60			65				

tat gtc ttc tcg gaa tac aac aggtcagagt gggccgacag ccctggggga 299
Tyr Val Phe Ser Glu Tyr Asn
70

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<210> 213
<211> 73
<212> PRT
<213> *Mus musculus*

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<400> 213
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      1       5       10      15

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Ser Gln Gly Ser Ala Arg Arg Pro Arg Pro Pro Lys Asp Pro Leu Arg
20 25 30

His Leu Arg Thr Arg Glu Lys Arg Gly Pro Gly Pro Gly Gly Pro Asn
35 40 45

Thr Val Tyr Leu Gln Val Val Ala Ala Gly Gly Arg Asp Ala Gly Ala
50 55 60

Ala Leu Tyr Val Phe Ser Glu Tyr Asn
65 70

<210> 214
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Histidine containing motif.

<220>
<221> SITE
<222> (1)..(3)
<223> These amino acids can each be any large hydrophobic residue.

<220>
<221> SITE
<222> (4)
<223> This is serine or threonine.

<220>
<221> SITE
<222> (6)
<223> This can be any amino acid residue.

<220>
<221> SITE
<222> (8)
<223> This can be any amino acid residue.

<220>
<221> SITE
<222> (11)..(12)
<223> These can be any amino acid residues.

<400> 214
Xaa Xaa Xaa Xaa His Xaa His Xaa Asp His Xaa Xaa Gly
1 5 10

<210> 215
<211> 127
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(127)
<223> Exon 1.

<400> 215
ttaatacga ctcactatag ggaatttggc cctcgagnng aattcggcac gagggtagcc 60
ccgcgacagc tgggccgagg gtgcgggcct cgcgtccctc ggctcctggc gcgggctcg 120
ggagagg 127

<210> 216
<211> 983
<212> DNA
<213> Homo sapiens

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<220>
<221> intron
<222> (1)..(300)
<223> Upstream intron of exon 2.

<220>
<221> misc_structure
<222> (301)..(465)
<223> Exon 2.

<220>
<221> intron
<222> (466)..(983)
<223> Intron downstream of exon 2.

<400> 216
gtctccatag tttgcctt ttgagaacat catatagta gaattcagct atagtttta 60
atgcctggg tttggtttatt ttgtttgtt tgggtgtgtg aacatttta caagattgt 120
taacttgtag ttttagccaa gttattaaaa ccttactgtg gatatgtgtg gaataactatg 180
agagaccaag aatccagact gttctaaata accaaaaagt aataatagag ataaatatta 240
caggaatatg tttttgtcc agtgtatga aataatcccc agatgtatct tctgttgcag 300
ggtggaaagat gtctatggat gtgacattcc tggggacggg tgcaagcatac ccattccaa 360
cccggggtgc ctctgtgtg gtcttcgtt gtgaaggcga gtgtggctc tttgactgt 420
gggagggaaac acagacacag cttatggaaa gcacacttaa agcaggtag tggcctca 480
gtatatctcat taagaatttt ttgttgttct gtctcatttt ctggctctc ctggacatt 540
ttgttagaa acagccctga tggttgcata ccacttcgt gctacaccct ggtgagactt 600
ggaaaggcctg caggcatctg gccacgtcca ctgacttca ttacttatt tacttgctt 660
tcatttatcc tgttagatgct gaaagcaagg attcatgttag gcttgggtt tggaaatgt 720
cgtggatacc accaggcata ttagatgaac actgccttag caaggaagca gtgtacatac 780
ttacccac caggagatag ttttcatgag aggatgcaaa ggtaggaaa tggtaggagg 840
aggagatgtt gtttccctct tggggtttac aggttaaactt ctcagagaag ttgacctgt 900
gattgtcaaa gagagagatt tcaggctgag agaagaaggc atttcatcag gggatggagt 960
gagcagagcc acacctggga gat 983

<210> 217
<211> 1287
<212> DNA
<213> Homo sapiens

<220>
<221> intron
<222> (1)..(300)
<223> Intron upstream of exon 3.

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<220>
 <221> misc_feature
 <222> (301)..(768)
 <223> Exon 3.

 <220>
 <221> intron
 <222> (769)..(1287)
 <223> Intron downstream of exon 3.

 <400> 217
 gtgagctatg atcacaccac tgcactccag cctggatgac agagcaagac ctgtctctt 60
 aaaaaaaaaa aaactattaa aaacaaacaa acaaaaaacc acctgggtcaa ataaaggctg 120
 tcttcttgg tttggaatca ttagcaaaa tgtaatgaa taagttatg atgataagta 180
 gaactttaa attcaattta ctatTTAA tgtaatttg taggcttgg tcaaataatgc 240
 ttgtatgggt tttagttaa tgaaaaattt ccaaacgtat tctcttatct caatcaaaag 300
 ggagaattac caagatctc atcacacacc ttcatggaga ccatttctt ggcttcctg 360
 ggcttccttg cacaaatcgc ctgcagagtg gctccatggt gtccaaacag cctattgaa 420
 tctatggccc tggtagggctt cgggacttta tctggcgaac catggaactc ttcacacgg 480
 agctggctt ccattatgtg gttcatgaac tggttccctac acgagatcaa tgcctgcag 540
 aagaactaaa agaatttgcg catgtgaata gagcagacag tcctcccaa gaggacaag 600
 gaagaactat cctgttagac tcagaagaaa actcataacct tctgtttgat gatgaacaat 660
 ttgttgtaaa agcatttgcg ctctttcaca gaattccctc atttgggtt tcaagtctgg 720
 aaaagaaaacg cccaggtaaa ctaatgcac agaaaacttaa agaccttggt aagtgtttt 780
 ttgttttttg tttttcccg ctttctcata aataggcctc ctgttgactg aagctataag 840
 aaatgtcata gtaaggccag gagttgtggc tcaacgctgt aatcttagca ctggggagg 900
 ccgaggtggg aggatcactt gagttcggga gttcaagacc agcctggca acatggcga 960
 accccatctc tactaaaaat acaaaaaagta actgggtgtg gtgtcatgtg cctgttagcc 1020
 cagctactt gggggctgag gcaggaggat cacttgaacc tgggaggtca aggctgcagt 1080
 aagccaaagat agtgttacta tactccagct tgggtgacaa acgcaaaactc tgcctcaaaa 1140
 aaaaaaaaaagt gtcatagtaa gttccactc ctctatccca ggcctgaaac tgacaatttc 1200
 tcacttagtc ctgtgtccaa agttgtttat taagaaaatcc atggggccaa aaaaatgcta 1260
 ttttagagcaa acccagttata catttga 1287

<210> 218
 <211> 1378
 <212> DNA
 <213> Homo sapiens

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<220>
<221> intron
<222> (1)..(300)
<223> Intron upstream of exon 4.

<220>
<221> misc_feature
<222> (301)..(966)
<223> Exon 4 with CDS ending at 764.

<220>
<221> intron
<222> (967)..(1378)
<223> Intron downstream of exon 4.

<400> 218
tgcacacg agagaatcaa gaatgttaca gtgactacaa taagtccta gtgatactta 60
ggagactaaa acttgtctga catgtatgca tggaaatgt ttcaagtact aaggcattgc 120
taatatcaat caacactgaa attttaaaaa tgtataatc cagtttcca caagtagtaa 180
aacatttata acaatttatgg atgcctttc cattagctat ttgcaatgct gttaaaatag 240
actcttgaaa agtcataaat tccatttcata tgatgtatg ttatctgcct tcattcattag 300
gtgtccacc aggtccctgcc tatggaaagc tgaaaaatgg aatttctgtt gttctggaaa 360
atggggttac aatttctccc caagatgtct taaaaaaagcc tattttgttga agaaaaatct 420
gcataattggg tgactgctct ggggttgtgg gtatggagg agtaaaactg tgcttgaag 480
cagacctgtt gatccacgaa gcaaccctgg atgatgccca gatggacaaa gcaaaggagc 540
atggccacag cacaccacag atggcagcaa catttgc当地 gttgtccgt gcaaaggagc 600
tggttctgac tcacttcagt cagaggtaa aaccaggc当地 ctggccaga gaaggagaaa 660
cagatggcat tgcagaacta aaaaagcaag ctgaatcagt gttagatctc caagaagtga 720
ctctagcaga agatttatg gtgataagca ttccaatcaa gaaatgaaac cagtttgc当地 780
gagtgacac tgacatgtct gtgaaatgt tactgaacct atagtc当地 ctttttattt 840
cttggggccct aataatcata aaaagaatgg agctgc当地 900
atgaattggc tcagtttta aaggagcaa accttttgc当地 aataatctt tttaagagaaa 960
aaaaaaaaacca gcatccctt tgaagtccag atttgc当地 aatgatagact attc当地 gttt 1020
.acattttattt ttgtgtact accacagata gccaatattc catgc当地 gtc当地 tggggccct 1080
ttctgccc当地 cttttttgc当地 gctattggca aagagcacag gactc当地 gagcc tcgtggccata 1140
aaatggtatt ttggcagttt gtattgtatc tggttgc当地 attaacagaa gagggagaaa 1200
tgctcatgaga cggtggacag gcaggattga tgatagcatg accatagctt tgctggaaata 1260
ctgaatgc当地 gagtttggca ggtgttattt ttaacattt attaaactt ctatggggt 1320
cttaaccat gggttctcaac tggggtgaca ctgc当地 cctct agaacaggta gaaatatg 1378

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<210> 219
 <211> 1462
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> (136)..(1224)

 <400> 219
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 ccgcacagc tggcccgagg gtgcggggct gcgcgtccctc ggctcttggc gccccgtcg 120
 ggagaggggt ggaag atg tct atg gat gtg aca ttc ctg ggg acg ggt gca 171
 Met Ser Met Asp Val Thr Phe Leu Gly Thr Gly Ala
 1 5 10

 gca tac cca tct cca acc cgg ggt gcc tct gct gtg gtc ctt cgg tgt 219
 Ala Tyr Pro Ser Pro Thr Arg Gly Ala Ser Ala Val Val Leu Arg Cys
 15 20 25

 gaa ggc gag tgc tgg ctc ttt gac tgg ggg gag gga aca cag aca cag 267
 Glu Gly Glu Cys Trp Leu Phe Asp Cys Gly Glu Gly Thr Gln Thr Gln
 30 35 40

 ctt atg aaa agc caa ctt aaa gca ggg aga att acc aag atc ttc atc 315
 Leu Met Lys Ser Gln Leu Lys Ala Gly Arg Ile Thr Lys Ile Phe Ile
 45 50 55 60

 aca cac ctt cat gga gac cat ttc ttt ggc ctt cct ggg ctc ctc tgc 363
 Thr His Leu His Gly Asp His Phe Phe Gly Leu Pro Gly Leu Leu Cys
 65 70 75

 aca atc agc ctg cag agt ggc tcc atg gtg tcc aaa cag cct att gaa 411
 Thr Ile Ser Leu Gln Ser Gly Ser Met Val Ser Lys Gln Pro Ile Glu
 80 85 90

 atc tat ggc cct gta ggg ctt cggt gac ttt atc tgg cga acc atg gaa 459
 Ile Tyr Gly Pro Val Gly Leu Arg Asp Phe Ile Trp Arg Thr Met Glu
 95 100 105

 ctc tct cac acg gag ctg gtc ttc cat tat gtg gtt cat gaa ctg gtt 507
 Leu Ser His Thr Glu Leu Val Phe His Tyr Val Val His Glu Leu Val
 110 115 120

 cct aca gca gat caa tgt cct gca gaa gaa cta aaa gaa ttt ggc cat 555
 Pro Thr Ala Asp Gln Cys Pro Ala Glu Glu Leu Lys Glu Phe Ala His
 125 130 135 140

 gtg aat aga gca gac agt cct ccc aaa gag gaa caa gga aga act atc 603
 Val Asn Arg Ala Asp Ser Pro Pro Lys Glu Glu Gln Gly Arg Thr Ile
 145 150 155

 ctg tta gac tca gaa gaa aac tca tac ctt ctg ttt gat gat gaa caa 651
 Leu Leu Asp Ser Glu Glu Asn Ser Tyr Leu Leu Phe Asp Asp Glu Gln
 160 165 170

 ttt gtt gta aaa gca ttt cgc ctc ttt cac aga att ccc tca ttt ggg 699
 Phe Val Val Lys Ala Phe Arg Leu Phe His Arg Ile Pro Ser Phe Gly
 175 180 185

tca gtc gtg gaa aag aaa cgc cca ggt aaa ctc aat gca cag aaa	747
Phe Ser Val Val Glu Lys Lys Arg Pro Gly Lys Leu Asn Ala Gin Lys	
190 195 200	
ttt aaa gac ctt ggt gtt cca cca ggt cct gcc tat ggg aag ctg aaa	795
Leu Lys Asp Leu Gly Val Pro Pro Gly Pro Ala Tyr Gly Lys Leu Lys	
205 210 215 220	
aat gga att tct gtt gtt ctg gaa aat ggg gtt aca att tct ccc caa	843
Asn Gly Ile Ser Val Val Leu Glu Asn Gly Val Thr Ile Ser Pro Gln	
225 230 235	
gat gtc tta aaa aag cct att gtt gga aga aaa atc tgc ata ttg ggt	891
Asp Val Leu Lys Lys Pro Ile Val Gly Arg Lys Ile Cys Ile Leu Gly	
240 245 250	
gac tgc tct ggg gtt gtg ggt gat gga gga gta aaa ctg tgc ttt gaa	939
Asp Cys Ser Gly Val Val Gly Asp Gly Val Lys Leu Cys Phe Glu	
255 260 265	
gca gac ctg ttg atc cac gaa gca acc ctg gat gat gcc cag atg gac	987
Ala Asp Leu Leu Ile His Glu Ala Thr Leu Asp Asp Ala Gln Met Asp	
270 275 280	
aaa gca aag gag cat ggc cac agc aca cca cag atg gca gca aca ttt	1035
Lys Ala Lys Glu His Gly His Ser Thr Pro Gln Met Ala Ala Thr Phe	
285 290 295 300	
gca aag ttg tgc cgt gca aag agg ctg gtt ctg act cac ttc agt cag	1083
Ala Lys Leu Cys Arg Ala Lys Arg Leu Val Leu Thr His Phe Ser Gln	
305 310 315	
agg tac aaa cca gtt gcc ttg gcc aga gaa gga gaa aca gat ggc att	1131
Arg Tyr Lys Pro Val Ala Leu Ala Arg Glu Gly Glu Thr Asp Gly Ile	
320 325 330	
gca gaa cta aaa aag caa gct gaa tca gtg tta gat ctc caa gaa gtg	1179
Ala Glu Leu Lys Lys Gln Ala Glu Ser Val Leu Asp Leu Gln Glu Val	
335 340 345	
act cta gca gaa gat ttt atg gtg ata agc att cca atc aag aaa	1224
Thr Leu Ala Glu Asp Phe Met Val Ile Ser Ile Pro Ile Lys Lys	
350 355 360	
tgaaaccagt gttcctgagt gcacactgac atgtctgtga atatgttact gaacctatag	1284
ttccagtttt ttatattctt ttttagtctg aaattatttg ggccctaata atccaaaaaa	1344
gaatggagct gcattgtatga attggctcag tatttaaagg gagcaaactt tttgataata	1404
aatctttta agagaaaaaa aaaaaaaaaa aaaaagatct ataattaagc agggggcat	1462
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<211> 363	
<212> PRT	
<213> Homo sapiens	
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Pro Thr Arg Gly Ala Ser Ala Val Val Leu Arg Cys Glu Gly Glu Cys
 20 25 30

Trp Leu Phe Asp Cys Gly Glu Gly Thr Gln Thr Gln Leu Met Lys Ser
 35 40 45

Gln Leu Lys Ala Gly Arg Ile Thr Lys Ile Phe Ile Thr His Leu His
 50 55 60

Gly Asp His Phe Phe Gly Leu Pro Gly Leu Leu Cys Thr Ile Ser Leu
 65 70 75 80

Gln Ser Gly Ser Met Val Ser Lys Gln Pro Ile Glu Ile Tyr Gly Pro
 85 90 95

Val Gly Leu Arg Asp Phe Ile Trp Arg Thr Met Glu Leu Ser His Thr
 100 105 110

Glu Leu Val Phe His Tyr Val Val His Glu Leu Val Pro Thr Ala Asp
 115 120 125

Gln Cys Pro Ala Glu Glu Leu Lys Glu Phe Ala His Val Asn Arg Ala
 130 135 140

Asp Ser Pro Pro Lys Glu Glu Gln Gly Arg Thr Ile Leu Leu Asp Ser
 145 150 155 160

Glu Glu Asn Ser Tyr Leu Leu Phe Asp Asp Glu Gln Phe Val Val Lys
 165 170 175

Ala Phe Arg Leu Phe His Arg Ile Pro Ser Phe Gly Phe Ser Val Val
 180 185 190

Glu Lys Lys Arg Pro Gly Lys Leu Asn Ala Gln Lys Leu Lys Asp Leu
 195 200 205

Gly Val Pro Pro Gly Pro Ala Tyr Gly Lys Leu Lys Asn Gly Ile Ser
 210 215 220

Val Val Leu Glu Asn Gly Val Thr Ile Ser Pro Gln Asp Val Leu Lys
 225 230 235 240

Lys Pro Ile Val Gly Arg Lys Ile Cys Ile Leu Gly Asp Cys Ser Gly
 245 250 255

Val Val Gly Asp Gly Gly Val Lys Leu Cys Phe Glu Ala Asp Leu Leu
 260 265 270

Ile His Glu Ala Thr Leu Asp Asp Ala Gln Met Asp Lys Ala Lys Glu
 275 280 285

His Gly His Ser Thr Pro Gln Met Ala Ala Thr Phe Ala Lys Leu Cys
 290 295 300

Arg Ala Lys Arg Leu Val Leu Thr His Phe Ser Gln Arg Tyr Lys Pro
 305 310 315 320

Val Ala Leu Ala Arg Glu Gly Glu Thr Asp Gly Ile Ala Glu Leu Lys
 325 330 335

Lys Gln Ala Glu Ser Val Leu Asp Leu Gln Glu Val Thr Leu Ala Glu
 340 345 350

Asp Phe Met Val Ile Ser Ile Pro Ile Lys Lys
 355 360

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<211> 2470
<212> DNA
<213> Mus musculus

<220>
<221> CDS
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<400> 221
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Met Trp Ala Leu Arg Ser Leu Leu Arg Pro Leu Gly Leu Arg Thr Met
 1 5 10 15

tcg cag ggt tcg gct cgt cgg cgg cca ccc aaa gac cca ctg cga 96
Ser Gln Gly Ser Ala Arg Arg Pro Arg Pro Pro Lys Asp Pro Leu Arg
 20 25 30

cac ctg cgt acg cgg gag aag cgc gcc cgg ggt ccc ggg ggc cgg aac 144
His Leu Arg Thr Arg Glu Lys Arg Gly Pro Gly Pro Gly Pro Asn
 35 40 45

acc gtg tac ctg cag gtg gtg gcg ggc cgg gac gcg ggg gct 192
Thr Val Tyr Leu Gln Val Ala Ala Gly Gly Arg Asp Ala Gly Ala
 50 55 60

gct ctc tat gtc ttc tcc gaa tac aac agg tac ctt ttt aac tgc gga 240
Ala Leu Tyr Val Phe Ser Glu Tyr Asn Arg Tyr Leu Phe Asn Cys Gly
 65 70 75 80

gaa ggc gtc caa cga ctt atg cag gaa cac aag act gaa agt cgc tcg 288
Glu Gly Val Gln Arg Leu Met Gln Glu His Lys Thr Glu Ser Arg Ser
 85 90 95

ctt gac aac atc ttt ctg act cgg atg cat tgg tca aat gtt ggg ggg 336
Leu Asp Asn Ile Phe Leu Thr Arg Met His Trp Ser Asn Val Gly Gly
 100 105 110

ttg tgt gga atg att tta act tta aag gaa acc ggg ctt ccc aaa tgt 384
Leu Cys Gly Met Ile Leu Thr Leu Lys Glu Thr Gly Leu Pro Lys Cys
 115 120 125

gtt ctg tct gga cca cca cag ctg gag aaa tat cta gaa gca atc aaa 432
Val Leu Ser Gly Pro Pro Gln Leu Glu Lys Tyr Leu Glu Ala Ile Lys
 130 135 140

ata ttt tct ggt cca ttg aaa gga ata gaa ctg gcc gtg cgg cct cac 480
Ile Phe Ser Gly Pro Leu Lys Gly Ile Glu Leu Ala Val Arg Pro His
 145 150 155 160

tct gca cca gaa tac aag gat gag acc atg act gtt tac cag gtc cct 528
Ser Ala Pro Glu Tyr Lys Asp Glu Thr Met Thr Val Tyr Gln Val Pro
 165 170 175

atc cac agt gaa cgg agg tgt gga aag caa cag cca tcc cag agc ccc 576
Ile His Ser Glu Arg Arg Cys Gly Lys Gln Gln Pro Ser Gln Ser Pro
 180 185 190

aga aca tct ccc aac agg ctc agt ccc aaa cag tca tcg gac tct gga	624
Arg Thr Ser Pro Asn Arg Leu Ser Pro Lys Gln Ser Ser Asp Ser Gly	
195	200
205	
tca gct gaa aat ggg cag tgc caa cag gaa agg atg ggg cag gga ccc	672
Ser Ala Glu Asn Gly Gln Cys Gln Gln Glu Ser Met Gly Gln Gly Pro	
210	215
220	
tcc tta gtg gta gct ttt gtc tgc aag ctt cac ttg agg aaa gga aac	720
Ser Leu Val Val Ala Phe Val Cys Lys Leu His Leu Arg Lys Gly Asn	
225	230
235	240
ttc ttg gtg ctt aaa gca aag gag ctg ggc ctt cct gtt ggg acg gcc	768
Phe Leu Val Leu Lys Ala Lys Glu Leu Gly Leu Pro Val Gly Thr Ala	
245	250
255	
gcc att gca ccc atc att gct gtc aag gac ggg aag agt atc act	816
Ala Ile Ala Pro Ile Ile Ala Ala Val Lys Asp Gly Lys Ser Ile Thr	
260	265
270	
tac gaa gga aga gag att gct gct gaa gag ctt tgt aca ccc cca gat	864
Tyr Glu Gly Arg Glu Ile Ala Ala Glu Glu Leu Cys Thr Pro Pro Asp	
275	280
285	
cct ggt ctt gta ttc atc gtg gta gag tgt ctt gat gaa gga ttc atc	912
Pro Gly Leu Val Phe Ile Val Val Glu Cys Pro Asp Glu Gly Phe Ile	
290	295
300	
ctg ccc atc tgt gag aac gac acc ttt aaa agg tac cag gca gag gct	960
Leu Pro Ile Cys Glu Asn Asp Thr Phe Lys Arg Tyr Gln Ala Glu Ala	
305	310
315	320
gtt gca cct qtg qcq ctg qtg qtc cac ata gcc cca gaa tct gta ctc	1008
Asp Ala Pro Val Ala Leu Val Val His Ile Ala Pro Glu Ser Val Leu	
325	330
335	
atc gac agc aga tac cag cag tgg atg gag agg ttc ggg cct gac aca	1056
Ile Asp Ser Arg Tyr Gln Gln Trp Met Glu Arg Phe Gly Pro Asp Thr	
340	345
350	
cag cac ctg att ctg aat gag aat tgc ccc tcg gtc cac aac ctg cgc	1104
Gln His Leu Ile Leu Asn Glu Asn Cys Pro Ser Val His Asn Leu Arg	
355	360
365	
agg cac aag att cag acc cag ctc agc ctc atc cac cct gac atc ttc	1152
Ser His Lys Ile Gln Thr Gln Leu Ser Leu Ile His Pro Asp Ile Phe	
370	375
380	
ccc cag ctt acc agc ttc tat agt aag gag gaa ggg tcc acc ctc agc	1200
Pro Gln Leu Thr Ser Phe Tyr Ser Lys Glu Gly Ser Thr Leu Ser	
385	390
395	400
gtt cca aca gtt cgg ggt gaa tgc ctc ctc aag tat tca gtc cgc ccc	1248
Val Pro Thr Val Arg Gly Glu Cys Leu Leu Lys Tyr Ser Val Arg Pro	
405	410
415	
aag aga gag tgg cag agg gat acc aca ctc gac tgc aat act gat gaa	1296
Lys Arg Glu Trp Gln Arg Asp Thr Thr Leu Asp Cys Asn Thr Asp Glu	
420	425
430	
ttc ata gct gag gcc ttg gag ctc ccc agt ttc cag gag agt gtg gag	1344
Phe Ile Ala Glu Ala Leu Glu Leu Pro Ser Phe Gln Glu Ser Val Glu	
435	440
445	

gag tat cgg aac acg gtc cag gaa aac cca gcc cca gca gag aaa aga Tyr Arg Lys Asn Val Gln Glu Asn Pro Ala Pro Ala Glu Lys Arg 450 455 460	1392
acg cag tat cct gaa att gtc ttc ctg ggt acg ggg tct gcc atc cca Ser Gln Tyr Pro Glu Ile Val Phe Leu Gly Thr Gly Ser Ala Ile Pro 465 470 475 480	1440
atg gag atc cga aat gtc agt tcc aca ctc gtc aac cta agc cct gac Met Glu Ile Arg Asn Val Ser Ser Thr Leu Val Asn Leu Ser Pro Asp 485 490 495	1488
aag tca gtg ctc ctg gat tgt gga gaa ggc act ttt ggg cag ttg tgc Lys Ser Val Leu Leu Asp Cys Gly Gly Thr Phe Gly Gln Leu Cys 500 505 510	1536
cgt cat tac gga cag caa ata gac cga gtc tta tgc agc ctc acg gct Arg His Tyr Gly Gln Gln Ile Asp Arg Val Leu Cys Ser Leu Thr Ala 515 520 525	1584
gtg ttt gtg tcc cac ctg cac gcc gac cac acg ggc ttg ctg aat Val Phe Val Ser His Leu His Ala Asp His His Thr Gly Leu Leu Asn 530 535 540	1632
atc ttg ctg cag aga gag cat gcg ttg gca tct ctg ggg aaa ccc ttc Ile Leu Leu Gln Arg Glu His Ala Leu Ala Ser Leu Gly Lys Pro Phe 545 550 555 560	1680
cag ccc ttg ctt gtg gtg gct cct acc cag ctc agg gcc tgg ctg cag Gln Pro Leu Leu Val Val Ala Pro Thr Gln Leu Arg Ala Trp Leu Gln 565 570 575	1728
cag tat cac aac cac tgc cag gag att ctg cac cac gtc agt atg att Gln Tyr His Asn His Cys Gln Glu Ile Leu His His Val Ser Met Ile 580 585 590	1776
cct gcc aaa tgc ctt cag aaa ggg gca gag gtc tcc aat act aca ttg Pro Ala Lys Cys Leu Gln Lys Gly Ala Glu Val Ser Asn Thr Thr Leu 595 600 605	1824
gaa agg ctg ata agc ttg ctg ttg gaa aca tgt gac tta gaa gaa tt Glu Arg Leu Ile Ser Leu Leu Glu Thr Cys Asp Leu Glu Glu Phe 610 615 620	1872
cag acc tgc ctg gta cgg cac tgc aag cat gct ttg ggc tgt gca ctg Gln Thr Cys Leu Val Arg His Cys Lys His Ala Phe Gly Cys Ala Leu 625 630 635 640	1920
gta cat tca tct ggc tgg aaa gtc gtc tac tcg ggg gat acc atg ccc Val His Ser Ser Gly Trp Lys Val Val Tyr Ser Gly Asp Thr Met Pro 645 650 655	1968
tgt gag gct ctg ctc cag atg ggg aaa gat gcc acc ctc ctg ata cat Cys Glu Ala Leu Val Gln Met Gly Lys Asp Ala Thr Leu Leu Ile His 660 665 670	2016
gaa gcc act ctg gag gat cnc ttg gaa gag gaa gca gta gag agg aca Glu Ala Thr Leu Glu Asp Xaa Leu Glu Glu Ala Val Glu Arg Thr 675 680 685	2064
cac agc acc acc tcc cag gct att aat gtg ggg atg cgg atg aat gcg His Ser Thr Thr Ser Gln Ala Ile Asn Val Gly Met Arg Met Asn Ala 690 695 700	2112

gag ttc atc atg ctg aac cac ttc agt cag cgg tac gcn aag atc ccc Glu Phe Ile Met Leu Asn His Phe Ser Gln Arg Tyr Xaa Lys Ile Pro 705 710 715 720	2160
ctt ttc agc cct gac ttc aac gag aaa gtt ggc atc gcc ttt gac cac Leu Phe Ser Pro Asp Phe Asn Glu Lys Val Gly Ile Ala Phe Asp His 725 730 735	2208
atg aag gtc tgn ttt gga gac ttc ccg aca gtg ccc aag ctg att ccc Met Lys Val Xaa Phe Gly Asp Phe Pro Thr Val Pro Lys Leu Ile Pro 740 745 750	2256
cca ctg aag gcc ctg ttt gca ggt gac att gaa gag atg gtg gaa cgc Pro Leu Lys Ala Leu Phe Ala Gly Asp Ile Glu Glu Met Val Glu Arg 755 760 765	2304
agg gag aag agg gag cta cgg ctg gtg cga gca gcc ctc ctg acc cag Arg Glu Lys Arg Glu Leu Arg Leu Val Arg Ala Ala Leu Leu Thr Gln 770 775 780	2352
cag gca gac agc cca gag gac aga gaa ccc caa cag aag cgg gcc cac Gln Ala Asp Ser Pro Glu Asp Arg Glu Pro Gln Lys Arg Ala His 785 790 795 800	2400
aca gat gaa cca cac agc cca cag agc aag aag gag agc gtg gca aac Thr Asp Glu Pro His Ser Pro Gln Ser Lys Lys Glu Ser Val Ala Asn 805 810 815	2448
act tta gga gcg cga gtg tgag Thr Leu Gly Ala Arg Val 820	2470
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His Leu Arg Thr Arg Glu Lys Arg Gly Pro Gly Pro Gly Pro Asn 35 40 45	
Thr Val Tyr Leu Gln Val Val Ala Ala Gly Gly Arg Asp Ala Gly Ala 50 55 60	
Ala Leu Tyr Val Phe Ser Glu Tyr Asn Arg Tyr Leu Phe Asn Cys Gly 65 70 75 80	
Glu Gly Val Gln Arg Leu Met Gln Glu His Lys Thr Glu Ser Arg Ser 85 90 95	
Leu Asp Asn Ile Phe Leu Thr Arg Met His Trp Ser Asn Val Gly Gly 100 105 110	
Leu Cys Gly Met Ile Leu Thr Leu Lys Glu Thr Gly Leu Pro Lys Cys 115 120 125	

Val Leu Ser Gly Pro Pro Gln Leu Glu Lys Tyr Leu Glu Ala Ile Lys
 130 135 140
 Ile Phe Ser Gly Pro Leu Lys Gly Ile Glu Leu Ala Val Arg Pro His
 145 150 155 160
 Ser Ala Pro Glu Tyr Lys Asp Glu Thr Met Thr Val Tyr Gln Val Pro
 165 170 175
 Ile His Ser Glu Arg Arg Cys Gly Lys Gln Gln Pro Ser Gln Ser Pro
 180 185 190
 Arg Thr Ser Pro Asn Arg Leu Ser Pro Lys Gln Ser Ser Asp Ser Gly
 195 200 205
 Ser Ala Glu Asn Gly Gln Cys Gln Glu Ser Met Gly Gln Gly Pro
 210 215 220
 Ser Leu Val Val Ala Phe Val Cys Lys Leu His Leu Arg Lys Gly Asn
 225 230 235 240
 Phe Leu Val Leu Lys Ala Lys Glu Leu Gly Leu Pro Val Gly Thr Ala
 245 250 255
 Ala Ile Ala Pro Ile Ile Ala Ala Val Lys Asp Gly Lys Ser Ile Thr
 260 265 270
 Tyr Glu Gly Arg Glu Ile Ala Ala Glu Glu Leu Cys Thr Pro Pro Asp
 275 280 285
 Pro Gly Leu Val Phe Ile Val Val Glu Cys Pro Asp Glu Gly Phe Ile
 290 295 300
 Leu Pro Ile Cys Glu Asn Asp Thr Phe Lys Arg Tyr Gln Ala Glu Ala
 305 310 315 320
 Asp Ala Pro Val Ala Leu Val Val His Ile Ala Pro Glu Ser Val Leu
 325 330 335
 Ile Asp Ser Arg Tyr Gln Gln Trp Met Glu Arg Phe Gly Pro Asp Thr
 340 345 350
 Gln His Leu Ile Leu Asn Glu Asn Cys Pro Ser Val His Asn Leu Arg
 355 360 365
 Ser His Lys Ile Gln Thr Gln Leu Ser Leu Ile His Pro Asp Ile Phe
 370 375 380
 Pro Gln Leu Thr Ser Phe Tyr Ser Lys Glu Glu Gly Ser Thr Leu Ser
 385 390 395 400
 Val Pro Thr Val Arg Gly Glu Cys Leu Leu Lys Tyr Ser Val Arg Pro
 405 410 415
 Lys Arg Glu Trp Gln Arg Asp Thr Thr Leu Asp Cys Asn Thr Asp Glu
 420 425 430
 Phe Ile Ala Glu Ala Leu Glu Leu Pro Ser Phe Gln Glu Ser Val Glu
 435 440 445
 Glu Tyr Arg Lys Asn Val Gln Glu Asn Pro Ala Pro Ala Glu Lys Arg
 450 455 460

Ser Gln Tyr Pro Glu Ile Val Phe Leu Gly Thr Gly Ser Ala Ile Pro
 465 470 475 480
 Met Glu Ile Arg Asn Val Ser Ser Thr Leu Val Asn Leu Ser Pro Asp
 485 490 495
 Lys Ser Val Leu Leu Asp Cys Gly Glu Gly Thr Phe Gly Gln Leu Cys
 500 505 510
 Arg His Tyr Gly Gln Gln Ile Asp Arg Val Leu Cys Ser Leu Thr Ala
 515 520 525
 Val Phe Val Ser His Leu His Ala Asp His His Thr Gly Leu Leu Asn
 530 535 540
 Ile Leu Leu Gln Arg Glu His Ala Leu Ala Ser Leu Gly Lys Pro Phe
 545 550 555 560
 Gln Pro Leu Leu Val Val Ala Pro Thr Gln Leu Arg Ala Trp Leu Gln
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 Gln Tyr His Asn His Cys Gln Glu Ile Leu His His Val Ser Met Ile
 580 585 590
 Pro Ala Lys Cys Leu Gln Lys Gly Ala Glu Val Ser Asn Thr Thr Leu
 595 600 605
 Glu Arg Leu Ile Ser Leu Leu Leu Glu Thr Cys Asp Leu Glu Glu Phe
 610 615 620
 Gln Thr Cys Leu Val Arg His Cys Lys His Ala Phe Gly Cys Ala Leu
 625 630 635 640
 Val His Ser Ser Gly Trp Lys Val Val Tyr Ser Gly Asp Thr Met Pro
 645 650 655
 Cys Glu Ala Leu Val Gln Met Gly Lys Asp Ala Thr Leu Leu Ile His
 660 665 670
 Glu Ala Thr Leu Glu Asp Xaa Leu Glu Glu Glu Ala Val Glu Arg Thr
 675 680 685
 His Ser Thr Thr Ser Gln Ala Ile Asn Val Gly Met Arg Met Asn Ala
 690 695 700
 Glu Phe Ile Met Leu Asn His Phe Ser Gln Arg Tyr Xaa Lys Ile Pro
 705 710 715 720
 Leu Phe Ser Pro Asp Phe Asn Glu Lys Val Gly Ile Ala Phe Asp His
 725 730 735
 Met Lys Val Xaa Phe Gly Asp Phe Pro Thr Val Pro Lys Leu Ile Pro
 740 745 750
 Pro Leu Lys Ala Leu Phe Ala Gly Asp Ile Glu Glu Met Val Glu Arg
 755 760 765
 Arg Glu Lys Arg Glu Leu Arg Leu Val Arg Ala Ala Leu Leu Thr Gln
 770 775 780
 Gln Ala Asp Ser Pro Glu Asp Arg Glu Pro Gln Gln Lys Arg Ala His
 785 790 795 800

Thr Asp Glu Pro His Ser Pro Gln Ser Lys Lys Glu Ser Val Ala Asn
 805 810 815

Thr Leu Gly Ala Arg Val
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<220>
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Met Trp Ala Leu Cys Ser Leu Leu Arg Ser Ala Ala Gly Arg Thr Met
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tcg cag gga cgc acc ata tcg cag gca ccc gcc cgc cgc gag cgg cgg 96
Ser Gln Gly Arg Thr Ile Ser Gln Ala Pro Ala Arg Arg Glu Arg Pro
. 20 . 25 . 30

cgc aag gac ccg ctg cgg cac ctg cgc acg cga gag aag cgc gga ccg 144
Arg Lys Asp Pro Leu Arg His Leu Arg Thr Arg Glu Lys Arg Gly Pro
. 35 . 40 . 45

tcg ggg tgc tcc ggc ggc cca aac acc gtg tac ctg cag gtg gtg gca 192
Ser Gly Cys Ser Gly Gly Pro Asn Thr Val Tyr Leu Gln Val Val Ala
. 50 . 55 . 60

ggc ggt agc ccg gac tcg ggc gcc gcg ctc tac gtc ttc tcc gag ttc 240
Ala Gly Ser Arg Asp Ser Gly Ala Ala Leu Tyr Val Phe Ser Glu Phe
. 65 . 70 . 75 . 80

aac ccg tat ctc ttc aac tgt gga gaa ggc att cag aga ctc atg cag 288
Asn Arg Tyr Leu Phe Asn Cys Gly Glu Gly Ile Gln Arg Leu Met Gln
. 85 . 90 . 95

gag cac aag tta aag gtt gct cgc ctg gac aac ata ttc ctg aca cga 336
Glu His Lys Leu Lys Val Ala Arg Leu Asp Asn Ile Phe Leu Thr Arg
. 100 . 105 . 110

atg cac tgg tct aat gtt ggg ggc tta agt gga atg att ctt act tta 384
Met His Trp Ser Asn Val Gly Leu Ser Gly Met Ile Leu Thr Leu
. 115 . 120 . 125

aag gaa acc ggg ctt cca aag tgt gta ctt tct gga cct cca caa ctg 432
Lys Glu Thr Gly Leu Pro Lys Cys Val Leu Ser Gly Pro Pro Gln Leu
. 130 . 135 . 140

gaa aaa tac ctc gaa gca atc aaa ata ttt tct ggt cca ttg aaa gga 480
Glu Lys Tyr Leu Glu Ala Ile Lys Ile Phe Ser Gly Pro Leu Lys Gly
. 145 . 150 . 155 . 160

ata gaa ctg gct gtg cgg ccc cac tct gcc cca gaa tac gag gat gaa 528
Ile Glu Leu Ala Val Arg Pro His Ser Ala Pro Glu Tyr Glu Asp Glu
. 165 . 170 . 175

acc atg aca gtt tac cag atc ccc ata cac agt gaa cag agg agg gga 576
Thr Met Thr Val Tyr Gln Ile Pro Ile His Ser Glu Gln Arg Arg Gly
. 180 . 185 . 190

aag cac caa cca tgg cag agt cca gaa agg cct ctc agc agg ctc agt Lys His Gln Pro Trp Gln Ser Pro Glu Arg Pro Leu Ser Arg Leu Ser 195 200 205	624
cca gag cga tct tca gac tcc gag tca aat gaa aat gag cca cac ctt Pro Glu Arg Ser Ser Asp Ser Glu Ser Asn Glu Asn Glu Pro His Leu 210 215 220	672
cca cat ggt gtt agc cag aca aca ggg gtc agg gag tct tcc ctg gtc Pro His Gly Val Ser Gln Arg Arg Gly Val Arg Asp Ser Ser Leu Val 225 230 235 240	720
gtt gct ttc atc tgt aag ctt cac tta aag aca gga aac ttc ttg gtg Val Ala Phe Ile Cys Lys Leu His Leu Lys Arg Gly Asn Phe Leu Val 245 250 255	768
ctc aaa gca aag gag atg ggc ctc cca gtt ggg aca gct gcc atc gct Leu Lys Ala Lys Glu Met Gly Leu Pro Val Gly Thr Ala Ala Ile Ala 260 265 270	816
ccc atc att gct gtc aag gag ggg aac agc atc act cat gaa gga Pro Ile Ile Ala Ala Val Lys Asp Gly Lys Ser Ile Thr His Glu Gly 275 280 285	864
aga gag att ttg gct gaa gag ctg tgt act cct cca gat cct ggt gct Arg Glu Ile Leu Ala Glu Glu Leu Cys Thr Pro Pro Asp Pro Gly Ala 290 295 300	912
gct ttt gtg gtg gta gaa tgt cca gat gaa agc ttc att caa ccc atc Ala Phe Val Val Glu Cys Pro Asp Glu Ser Phe Ile Gln Pro Ile 305 310 315 320	960
tgt gag aat gcc acc ttt cag agg tac caa gga aag gca gat gcc ccc Cys Glu Asn Ala Thr Phe Gln Arg Tyr Gln Gly Lys Ala Asp Ala Pro 325 330 335	1008
gtg gcc ttg gtg gtt cac atg gcc cca gaa tct gtg ctt gtg gac agc Val Ala Leu Val Val His Met Ala Pro Glu Ser Val Leu Val Asp Ser 340 345 350	1056
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acc agt ttc ccc tgt aag aag gag ggc ccc acc ctc agt gtg ccc atg Thr Ser Phe Pro Cys Lys Lys Glu Gly Pro Thr Leu Ser Val Pro Met 405 410 415	1248
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tgg cag agg gat gcc att att act tgc aat cct gag gaa ttc ata att Trp Gln Arg Asp Ala Ile Ile Thr Cys Asn Pro Glu Glu Phe Ile Ile 435 440 445	1344

gag ggc ctg cag ctt ccc aac ttc cag cag agt gtg cag gag tac agg Glu Ala Leu Gln Leu Pro Asn Phe Gln Gln Ser Val Gln Glu Tyr Arg 450 455 460	1392
agg agt ggc cag gac ggc cca gca gca gag aaa aga agt cag tac Arg Ser Ala Gln Asp Gly Pro Ala Pro Ala Glu Lys Arg Ser Gln Tyr 465 470 475 480	1440
cca gaa atc atc ttc ctt gga aca ggg tct gcc atc ccg atg aag att Pro Glu Ile Ile Phe Leu Gly Thr Gly Ser Ala Ile Pro Met Lys Ile 485 490 495	1488
cga aat gtc agt gcc aca ctt gtc aac ata agc ccc gac acg tct ctg Arg Asn Val Ser Ala Thr Leu Val Asn Ile Ser Pro Asp Thr Ser Leu 500 505 510	1536
cta ctg gac tgt ggt gag ggc agc ttt ggg cag ctg tgc cgt cat tac Leu Leu Asp Cys Gly Glu Gly Thr Phe Gly Gln Leu Cys Arg His Tyr 515 520 525	1584
gga gac cag gtg gac agg gtc ctg ggc acc ctg gct gct gtg ttt gtg Gly Asp Gln Val Asp Arg Val Leu Gly Thr Leu Ala Ala Val Phe Val 530 535 540	1632
tcc cac ctg cac gca gat cac cac acg ggc ttg cta aat atc ttg ctg Ser His Leu His Ala Asp His His Thr Gly Leu Leu Asn Ile Leu Leu 545 550 555 560	1680
cag aga gaa cga gcc ttg gca tct ttg gga aag ccc ttt cac cct ttg Gln Arg Glu Arg Ala Leu Ala Ser Leu Gly Lys Pro Phe His Pro Leu 565 570 575	1728
ctg gtc gtt gcc ccc aac cag ctc aaa gcc tgg ctc cag cag tac cac Leu Val Val Ala Pro Asn Gln Leu Lys Ala Trp Leu Gln Gln Tyr His 580 585 590	1776
aac cag tgc cag gag gtc ctg cac cac atc agt atg att cct gcc aaa Asn Gln Cys Gln Glu Val Leu His His Ile Ser Met Ile Pro Ala Lys 595 600 605	1824
tgc ctt cag gaa ggg gct gag atc tcc agt cct gca gtg gaa aga ttg Cys Leu Gln Glu Gly Ala Glu Ile Ser Ser Pro Ala Val Glu Arg Leu 610 615 620	1872
atc agt tcg ctg ttg cga aca tgt gat ttg gaa gag gac ttt cag acc tgt Ile Ser Ser Leu Leu Arg Thr Cys Asp Leu Glu Glu Phe Gln Thr Cys 625 630 635 640	1920
ctg gtg cgg cac tgc aag cat gcg ttt ggc tgt ggc ctg gtg cac acc Leu Val Arg His Cys Lys His Ala Phe Gly Cys Ala Leu Val His Thr 645 650 655	1968
tct ggc tgg aaa gtg gtc tat tcc ggg gac acc atg ccc tgc gag gct Ser Gly Trp Lys Val Val Tyr Ser Gly Asp Thr Met Pro Cys Glu Ala 660 665 670	2016
ctg gtc cgg atg ggg aaa gat gcc acc ctc ctg ata cat gaa gcc acc Leu Val Arg Met Gly Lys Asp Ala Thr Leu Leu Ile His Glu Ala Thr 675 680 685	2064
ctg gaa gac ggt ttg gaa gag gaa gca gtg gaa aag aca cac agc aca Leu Glu Asp Gly Leu Glu Glu Ala Val Glu Lys Thr His Ser Thr 690 695 700	2112

acg tcc caa gcc atc agc gtc ggg atg cgg atg aac gcg gag ttc att 2160
 Thr Ser Gln Ala Ile Ser Val Gly Met Arg Met Asn Ala Glu Phe Ile
 705 710 715 720
 atg ctg aac cac ttc agc cag cgc tat gcc aag gtc ccc ctc ttc agc 2208
 Met Leu Asn His Phe Ser Gln Arg Tyr Ala Lys Val Pro Leu Phe Ser
 725 730 735
 ccc aac ttc aac gag aaa gtc gga gtt gcc ttt gac cac atg aag gtc 2256
 Pro Asn Phe Asn Lys Val Gly Val Ala Phe Asp His Met Lys Val
 740 745 750
 tgc ttt gga gac ttt gca aca atg ccc aag ctg att ccc cca ctg aaa 2304
 Cys Phe Gly Asp Phe Ala Thr Met Pro Lys Leu Ile Pro Pro Leu Lys
 755 760 765
 gcc ctg ttt gct ggc gac atc gag gag atg gag gag gag cgcc agg gag aag 2352
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 770 775 780
 ccg gag ctg cgg cag gtc cgg gcg gcc ctc ctg tcc agg gag ctg gca 2400
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 785 790 795 800
 ggc ggc ctg gag gat ggg gag cct cag cag aaa cgg gcc cac aca gag 2448
 Gly Gly Leu Glu Asp Gly Glu Pro Gln Gln Lys Arg Ala His Thr Glu
 805 810 815
 gag cca cag gcc aag aag gtc aga gcc cag tgaagatctg ggagaccctg 2498
 Glu Pro Gln Ala Lys Lys Val Arg Ala Gln
 820 825
 aattcagaag gctgtgtgtc ttctgccccca cgcacgcacc cgtatctgcc ctcccttgctg 2558
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 caaggcattt ttaaagaag gttggaaaac agacggcagc acctttctc taatccagca 2798
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 Arg Lys Asp Pro Leu Arg His Leu Arg Thr Arg Glu Lys Arg Gly Pro
 35 40 45

Ser Gly Cys Ser Gly Gly Pro Asn Thr Val Tyr Leu Gln Val Val Ala
 50 55 60
 Ala Gly Ser Arg Asp Ser Gly Ala Ala Leu Tyr Val Phe Ser Glu Phe
 65 70 75 80
 Asn Arg Tyr Leu Phe Asn Cys Gly Glu Gly Ile Gin Arg Leu Met Gln
 85 90 95
 Glu His Lys Leu Lys Val Ala Arg Leu Asp Asn Ile Phe Leu Thr Arg
 100 105 110
 Met His Trp Ser Asn Val Gly Gly Leu Ser Gly Met Ile Leu Thr Leu
 115 120 125
 Lys Glu Thr Gly Leu Pro Lys Cys Val Leu Ser Gly Pro Pro Gln Leu
 130 135 140
 Glu Lys Tyr Leu Glu Ala Ile Lys Ile Phe Ser Gly Pro Leu Lys Gly
 145 150 155 160
 Ile Glu Leu Ala Val Arg Pro His Ser Ala Pro Glu Tyr Glu Asp Glu
 165 170 175
 Thr Met Thr Val Tyr Gln Ile Pro Ile His Ser Glu Gln Arg Arg Gly
 180 185 190
 Lys His Gln Pro Trp Gln Ser Pro Glu Arg Pro Leu Ser Arg Leu Ser
 195 200 205
 Pro Glu Arg Ser Ser Asp Ser Glu Ser Asn Glu Asn Glu Pro His Leu
 210 215 220
 Pro His Gly Val Ser Gln Arg Arg Gly Val Arg Asp Ser Ser Leu Val
 225 230 235 240
 Val Ala Phe Ile Cys Lys Leu His Leu Lys Arg Gly Asn Phe Leu Val
 245 250 255
 Leu Lys Ala Lys Glu Met Gly Leu Pro Val Gly Thr Ala Ala Ile Ala
 260 265 270
 Pro Ile Ile Ala Ala Val Lys Asp Gly Lys Ser Ile Thr His Glu Gly
 275 280 285
 Arg Glu Ile Leu Ala Glu Glu Leu Cys Thr Pro Pro Asp Pro Gly Ala
 290 295 300
 Ala Phe Val Val Val Glu Cys Pro Asp Glu Ser Phe Ile Gln Pro Ile
 305 310 315 320
 Cys Glu Asn Ala Thr Phe Gln Arg Tyr Gln Gly Lys Ala Asp Ala Pro
 325 330 335
 Val Ala Leu Val Val His Met Ala Pro Glu Ser Val Leu Val Asp Ser
 340 345 350
 Arg Tyr Gln Gln Trp Met Glu Arg Phe Gly Pro Asp Thr Gln His Leu
 355 360 365
 Val Leu Asn Glu Asn Cys Ala Ser Val His Asn Leu Arg Ser His Lys
 370 375 380

Ile Gln Thr Gln Leu Asn Leu Ile His Pro Asp Ile Phe Pro Leu Leu
 385 390 395 400

Thr Ser Phe Pro Cys Lys Lys Glu Gly Pro Thr Leu Ser Val Pro Met
 405 410 415

Val Gln Gly Glu Cys Leu Leu Lys Tyr Gln Leu Arg Pro Arg Arg Glu
 420 425 430

Trp Gln Arg Asp Ala Ile Ile Thr Cys Asn Pro Glu Glu Phe Ile Ile
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Glu Ala Leu Gln Leu Pro Asn Phe Gln Gln Ser Val Gln Glu Tyr Arg
 450 455 460

Arg Ser Ala Gln Asp Gly Pro Ala Pro Ala Glu Lys Arg Ser Gln Tyr
 465 470 475 480

Pro Glu Ile Ile Phe Leu Gly Thr Gly Ser Ala Ile Pro Met Lys Ile
 485 490 495

Arg Asn Val Ser Ala Thr Leu Val Asn Ile Ser Pro Asp Thr Ser Leu
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Leu Leu Asp Cys Gly Glu Gly Thr Phe Gly Gln Leu Cys Arg His Tyr
 515 520 525

Gly Asp Gln Val Asp Arg Val Leu Gly Thr Leu Ala Ala Val Phe Val
 530 535 540

Ser His Leu His Ala Asp His His Thr Gly Leu Leu Asn Ile Leu Leu
 545 550 555 560

Gln Arg Glu Arg Ala Leu Ala Ser Leu Gly Lys Pro Phe His Pro Leu
 565 570 575

Leu Val Val Ala Pro Asn Gln Leu Lys Ala Trp Leu Gln Gln Tyr His
 580 585 590

Asn Gln Cys Gln Glu Val Leu His His Ile Ser Met Ile Pro Ala Lys
 595 600 605

Cys Leu Gln Glu Gly Ala Glu Ile Ser Ser Pro Ala Val Glu Arg Leu
 610 615 620

Ile Ser Ser Leu Leu Arg Thr Cys Asp Leu Glu Glu Phe Gln Thr Cys
 625 630 635 640

Leu Val Arg His Cys Lys His Ala Phe Gly Cys Ala Leu Val His Thr
 645 650 655

Ser Gly Trp Lys Val Val Tyr Ser Gly Asp Thr Met Pro Cys Glu Ala
 660 665 670

Leu Val Arg Met Gly Lys Asp Ala Thr Leu Leu Ile His Glu Ala Thr
 675 680 685

Leu Glu Asp Gly Leu Glu Glu Glu Ala Val Glu Lys Thr His Ser Thr
 690 695 700

Thr Ser Gln Ala Ile Ser Val Gly Met Arg Met Asn Ala Glu Phe Ile
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Met Leu Asn His Phe Ser Gln Arg Tyr Ala Lys Val Pro Leu Phe Ser
 725 730 735
 Pro Asn Phe Asn Glu Lys Val Gly Val Ala Phe Asp His Met Lys Val
 740 745 750
 Cys Phe Gly Asp Phe Ala Thr Met Pro Lys Leu Ile Pro Pro Leu Lys
 755 760 765
 Ala Leu Phe Ala Gly Asp Ile Glu Glu Met Glu Glu Arg Arg Glu Lys
 770 775 780
 Arg Glu Leu Arg Gln Val Arg Ala Ala Leu Leu Ser Arg Glu Leu Ala
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 Glu Pro Gln Ala Lys Lys Val Arg Ala Gln
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 Ser Gln Gly Arg Thr Ile Ser Gln Ala Pro Ala Arg Arg Glu Arg Pro
 20 25 30

cgc aag gac ccg ctg cgg cac ctg cgc acg cga gag aag cgc gga cgg
 Arg Lys Asp Pro Leu Arg His Leu Arg Thr Arg Glu Lys Arg Gly Pro
 35 40 45

tcg ggg tgc tcc ggg ggc cca aac acc gtg tac ctg cag gtg gtg gca
 Ser Gly Cys Ser Gly Gly Pro Asn Thr Val Tyr Leu Gln Val Val Ala
 50 55 60

gcg ggt agc ccg gac tcg ggc gcc gcg ctc tac gtc ttc tcc gag ttc
 Ala Gly Ser Arg Asp Ser Gly Ala Ala Leu Tyr Val Phe Ser Glu Phe
 65 70 75 80

aac cgg tat ctc ttc aac tgt gga gaa ggc gtt cag aga ctc atg cag
 Asn Arg Tyr Leu Phe Asn Cys Gly Glu Gly Val Gln Arg Leu Met Gln
 85 90 95

gag cac aag tta aag gtt gtt cgc ctg gac aac ata ttc ctg aca cga
 Glu His Lys Leu Lys Val Val Arg Leu Asp Asn Ile Phe Leu Thr Arg
 100 105 110

atg cac tgg tct aat gtt ggg ggc tta agt gga atg att ctt act tta
 Met His Trp Ser Asn Val Gly Gly Leu Ser Gly Met Ile Leu Thr Leu
 115 120 125

aag gaa acc ggg ctt cca aag tgt gta ctt tct gga cct cca cag ctg		432	
Lys Glu Thr Gly Leu Pro Lys Cys Val Leu Ser Gly Pro Pro Gln Leu			
130	135	140	
gaa aaa tac ctc gaa gca atc aaa ata ttt tct ggt cca ttg aaa gga		480	
Glu Lys Tyr Leu Glu Ala Ile Lys Ile Phe Ser Gly Pro Leu Lys Gly			
145	150	155	160
ata gaa ctg gct gtg cgg ccc cac tct gcc cca gaa tac gag gat gaa		528	
Ile Glu Leu Ala Val Arg Pro His Ser Ala Pro Glu Tyr Glu Asp Glu			
165	170	175	
acc atg aca gtt tac cag atc ccc ata cac agt gaa cag agg agg gga		576	
Thr Met Thr Val Tyr Gln Ile Pro Ile His Ser Glu Gln Arg Arg Gly			
180	185	190	
agg cac caa cca tgg cag agt cca gaa agg cct ctc agc agg ctc agt		624	
Arg His Gln Pro Trp Gln Ser Pro Glu Arg Pro Leu Ser Arg Leu Ser			
195	200	205	
cca gag cga tct tca gac tcc gag tcg aat gaa aat gag cca cac ctt		672	
Pro Glu Arg Ser Ser Asp Ser Glu Ser Asn Glu Asn Glu Pro His Leu			
210	215	220	
cca cat ggt gtt agc cag aga aga ggg gtc agg gac tct tcc ctg gtc		720	
Pro His Gly Val Ser Gln Arg Arg Gly Val Arg Asp Ser Ser Leu Val			
225	230	235	240
gta gct ttc atc tgt aag ctt cac tta aag aga gga aac ttc ttg gtg		768	
Val Ala Phe Ile Cys Lys Leu His Leu Lys Arg Gly Asn Phe Leu Val			
245	250	255	
ctc aaa gca aag gag atg ggc ctc cca gtt ggg aca gct gcc atc gct		816	
Leu Lys Ala Lys Glu Met Gly Leu Pro Val Gly Thr Ala Ala Ile Ala			
260	265	270	
ccc atc att gct gtc aag gac ggg aaa agc atc act cat gaa gga		864	
Pro Ile Ile Ala Ala Val Lys Asp Gly Lys Ser Ile Thr His Glu Gly			
275	280	285	
aga gag att ttg gct gaa gag ctg tgt act cct cca gat cct ggt gct		912	
Arg Glu Ile Leu Ala Glu Glu Leu Cys Thr Pro Pro Asp Pro Gly Ala			
290	295	300	
gct ttt gtg gtg gta gaa tgt cca gat gaa agc ttc att caa ccc atc		960	
Ala Phe Val Val Glu Cys Pro Asp Glu Ser Phe Ile Gln Pro Ile			
305	310	315	320
tgt gag aat gcc acc ttt cag agg tac caa gga aag gca gat gcc ccc		1008	
Cys Glu Asn Ala Thr Phe Gln Arg Tyr Gln Gly Lys Ala Asp Ala Pro			
325	330	335	
gtg gcc ttg gtg gtt cac atg gcc cca gaa tct gtg ctt gtg gac agc		1056	
Val Ala Leu Val Val His Met Ala Pro Glu Ser Val Leu Val Asp Ser			
340	345	350	
agg tac cag cag tgg atg gag agg ttt ggg cct gac acc cag cac ttg		1104	
Arg Tyr Gln Gln Trp Met Glu Arg Phe Gly Pro Asp Thr Gln His Leu			
355	360	365	
gtc ctg aat gag aac ttt gtc tca gtt cac aac ctt cgc agc cac aag		1152	
Val Leu Asn Glu Asn Cys Ala Ser Val His Asn Leu Arg Ser His Lys			
370	375	380	

att caa acc cag ctc aac ctc atc cac ccg gac atc ttc ccc ctg ctc Ile Gln Thr Gln Leu Asn Leu Ile His Pro Asp Ile Phe Pro Leu Leu 385 390 395 400	1200
acc agt ttc ccc tgt aag aag gag ggc ccc acc ctc agt gtg ccc atg Thr Ser Phe Pro Cys Lys Lys Glu Gly Pro Thr Leu Ser Val Pro Met 405 410 415	1248
gtt cag ggt gaa tgc ctc ctc aag tac cag ctc cgt ccc agg agg gaa Val Gln Gly Cys Leu Leu Lys Tyr Gln Leu Arg Pro Arg Arg Glu 420 425 430	1296
tgg cag agg gat gcc att atc act tgc aat cct gag gaa ttc ata gtt Trp Gln Arg Asp Ala Ile Ile Thr Cys Asn Pro Glu Glu Phe Ile Val 435 440 445	1344
gag gcg ctg cag ctt ccc aac ttc cag cag agt gtg cag gag tac agg Glu Ala Leu Gln Leu Pro Asn Phe Gln Gln Ser Val Gln Glu Tyr Arg 450 455 460	1392
agg agt gtg cag gac gtc cca gcc cca gca gag aaa aga agt cag tac Arg Ser Val Gln Asp Val Pro Ala Pro Leu Lys Arg Ser Gln Tyr 465 470 475 480	1440
cca gaa atc atc ttc ctt gga aca ggg tct gcc atc ccc atg aag att Pro Glu Ile Ile Phe Leu Gly Thr Gly Ser Ala Ile Pro Met Lys Ile 485 490 495	1488
cga aat gtc agt gcc aca ctt gtc aac ata agc ccc gac acg tct ctg Arg Asn Val Ser Ala Thr Leu Val Asn Ile Ser Pro Asp Thr Ser Leu 500 505 510	1536
cta ctg gac tgt ggt gag ggc acg ttt ggg cag ctg tgc cgt cat tac Leu Leu Asp Cys Gly Glu Gly Thr Phe Gly Gln Leu Cys Arg His Tyr 515 520 525	1584
gga gac cag gtg gac agg gtc ctg ggc acc ctg gct gct gtg ttt gtg Gly Asp Gln Val Asp Arg Val Leu Gly Thr Leu Ala Ala Val Phe Val 530 535 540	1632
tcc cac ctg cac gca gat cac cac acg ggc ttg cta aat atc ttg ctg Ser His Leu His Ala Asp His His Thr Gly Leu Leu Asn Ile Leu Leu 545 550 555 560	1680
cag aga gaa caa gcc ttg gca tct ttg gga aag ccc ctt cac cct ttg Gln Arg Glu Gln Ala Leu Ala Ser Leu Gly Lys Pro Leu His Pro Leu 565 570 575	1728
ctg gtg gtt gcc ccc agc cag ctc aaa gcc tgg ctc cag cag tac cac Leu Val Val Ala Pro Ser Gln Leu Lys Ala Trp Leu Gln Gln Tyr His 580 585 590	1776
aac cag tgc cag gag gtc ctg cac cac atc agt atg att cct gcc aaa Asn Gln Cys Gln Glu Val Leu His His Ile Ser Met Ile Pro Ala Lys 595 600 605	1824
tgc ctt cag gaa ggg gct gag atc tcc agt cct gca gtg gaa aga ttg Cys Leu Gln Glu Gly Ala Glu Ile Ser Ser Pro Ala Val Glu Arg Leu 610 615 620	1872
atc agt tcg ctg ttg cga aca tgt gat ttg gaa gag ttt cag acc tgt Ile Ser Ser Leu Leu Arg Thr Cys Asp Leu Glu Glu Phe Gln Thr Cys 625 630 635 640	1920

ctg gtg cgg cac tgc aag cat gcg ttt ggc tgt gcg ctg gtg cac acc Leu Val Arg His Cys Lys His Ala Phe Gly Cys Ala Leu Val His Thr 645 650 655	1968
tct ggc tgg aaa gtg gtc tat tcc ggg gac atg ccc tgc gag gct Ser Gly Trp Lys Val Val Tyr Ser Gly Asp Thr Met Pro Cys Glu Ala 660 665 670	2016
ctg gtc cgc atg ggg aaa gat gcc acc ctc ctg ata cat gaa gcc acc Leu Val Arg Met Gly Lys Asp Ala Thr Leu Leu Ile His Glu Ala Thr 675 680 685	2064
ctg gaa gat ggt ttg gaa gag gaa gca gtg gaa aag aca cac agc aca Leu Glu Asp Gly Leu Glu Glu Ala Val Glu Lys Thr His Ser Thr 690 695 700	2112
acg tcc caa gcc atc aac gtg ggg atg cgg atg aac ggg gag ttc att Thr Ser Gln Ala Ile Ser Val Gly Met Arg Met Asn Ala Glu Phe Ile 705 710 715 720	2160
atg ctg aac cac ttc aac cag cgc tat gcc aag gtc ccc ctc ttc agc Met Leu Asn His Phe Ser Gln Arg Tyr Ala Lys Val Pro Leu Phe Ser 725 730 735	2208
ccc aac ttc aac gag aaa gtg gga gtt gcc ttt gac cac atg aag gtc Pro Asn Phe Asn Glu Lys Val Gly Val Ala Phe Asp His Met Lys Val 740 745 750	2256
tgc ttt gga gac ttt cca aca atg ccc aag ctg att ccc cca ctg aac Cys Phe Gly Asp Phe Pro Thr Met Pro Lys Leu Ile Pro Pro Leu Lys 755 760 765	2304
gcc ctg ttt gcc ggc gac atc gag gag atg gag gag cgc agg gag aag Ala Leu Phe Ala Gly Asp Ile Glu Glu Met Glu Arg Arg Glu Lys 770 775 780	2352
ccg gag ctg cgg cag gtg cgg ggc ctc ctg tcc ggg gag ctg gca Arg Glu Leu Arg Gln Val Arg Ala Ala Leu Leu Ser Gly Glu Leu Ala 785 790 795 800	2400
ggc ggc ctg gag gat ggg gag cct cag cag aaa cgg gcc cac aca gag Gly Gly Leu Glu Asp Gly Glu Pro Gln Gln Lys Arg Ala His Thr Glu 805 810 815	2448
gag cca cag gcc aag aag gtc aga gcc cag tgaatctg ggagaccctg Glu Pro Gln Ala Lys Lys Val Arg Ala Gln 820 825	2498
aattcagaag gctgtgtgtc ttctgccccca cgcacgcacc cgtatctgcc ctcccttgctg 2558 gttagaaacctg aagagcacgg tcccccaagga ggcagctcaag gataagggtgt atggagctgt 2618 ggcgaggcctt aggctccac ataagcacta gtctataatggt gcctggcaca gcccggggac 2678 aggaggctgc cacacggaaag caagcagatg aactaatttc atttcaaggc agtttttaaa 2738 gaagtcttgg aaacacgacgg cagcacctt cctctaattc agcaaagtga ttccctgcac 2798 accagagaca agcagagataa caggatcaat gggctcaatgt gtcccgagact taacaaaaat 2858 agtatccatcg ctgcaataaa gatttagttt gcaa	2892

<210> 226
 <211> 826
 <212> PRT
 <213> Gorilla gorilla

<400> 226
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Ser Gln Gly Arg Thr Ile Ser Gln Ala Pro Ala Arg Arg Glu Arg Pro
 20 25 30

Arg Lys Asp Pro Leu Arg His Leu Arg Thr Arg Glu Lys Arg Gly Pro
 35 40 45

Ser Gly Cys Ser Gly Gly Pro Asn Thr Val Tyr Leu Gln Val Val Ala
 50 55 60

Ala Gly Ser Arg Asp Ser Gly Ala Ala Leu Tyr Val Phe Ser Glu Phe
 65 70 75 80

Asn Arg Tyr Leu Phe Asn Cys Gly Glu Gly Val Gln Arg Leu Met Gln
 85 90 95

Glu His Lys Leu Lys Val Val Arg Leu Asp Asn Ile Phe Leu Thr Arg
 100 105 110

Met His Trp Ser Asn Val Gly Leu Ser Gly Met Ile Leu Thr Leu
 115 120 125

Lys Glu Thr Gly Leu Pro Lys Cys Val Leu Ser Gly Pro Pro Gln Leu
 130 135 140

Glu Lys Tyr Leu Glu Ala Ile Lys Ile Phe Ser Gly Pro Leu Lys Gly
 145 150 155 160

Ile Glu Leu Ala Val Arg Pro His Ser Ala Pro Glu Tyr Glu Asp Glu
 165 170 175

Thr Met Thr Val Tyr Gln Ile Pro Ile His Ser Glu Gln Arg Arg Gly
 180 185 190

Arg His Gln Pro Trp Gln Ser Pro Glu Arg Pro Leu Ser Arg Leu Ser
 195 200 205

Pro Glu Arg Ser Ser Asp Ser Glu Ser Asn Glu Asn Glu Pro His Leu
 210 215 220

Pro His Gly Val Ser Gln Arg Arg Gly Val Arg Asp Ser Ser Leu Val
 225 230 235 240

Val Ala Phe Ile Cys Lys Leu His Leu Lys Arg Gly Asn Phe Leu Val
 245 250 255

Leu Lys Ala Lys Glu Met Gly Leu Pro Val Gly Thr Ala Ala Ile Ala
 260 265 270

Pro Ile Ile Ala Ala Val Lys Asp Gly Lys Ser Ile Thr His Glu Gly
 275 280 285

Arg Glu Ile Leu Ala Glu Glu Leu Cys Thr Pro Pro Asp Pro Gly Ala
 290 295 300

Ala Phe Val Val Val Glu Cys Pro Asp Glu Ser Phe Ile Gln Pro Ile
 305 310 315 320
 Cys Glu Asn Ala Thr Phe Gln Arg Tyr Gln Gly Lys Ala Asp Ala Pro
 325 330 335
 Val Ala Leu Val Val His Met Ala Pro Glu Ser Val Leu Val Asp Ser
 340 345 350
 Arg Tyr Gln Gln Trp Met Glu Arg Phe Gly Pro Asp Thr Gln His Leu
 355 360 365
 Val Leu Asn Glu Asn Cys Ala Ser Val His Asn Leu Arg Ser His Lys
 370 375 380
 Ile Gin Thr Gln Leu Asn Leu Ile His Pro Asp Ile Phe Pro Leu Leu
 385 390 395 400
 Thr Ser Phe Pro Cys Lys Lys Glu Gly Pro Thr Leu Ser Val Pro Met
 405 410 415
 Val Gin Gly Glu Cys Leu Leu Lys Tyr Gln Leu Arg Pro Arg Arg Glu
 420 425 430
 Trp Gln Arg Asp Ala Ile Ile Thr Cys Asn Pro Glu Glu Phe Ile Val
 435 440 445
 Glu Ala Leu Gln Leu Pro Asn Phe Gln Gln Ser Val Gln Glu Tyr Arg
 450 455 460
 Arg Ser Val Gln Asp Val Pro Ala Pro Ala Glu Lys Arg Ser Gln Tyr
 465 470 475 480
 Pro Glu Ile Ile Phe Leu Gly Thr Gly Ser Ala Ile Pro Met Lys Ile
 485 490 495
 Arg Asn Val Ser Ala Thr Leu Val Asn Ile Ser Pro Asp Thr Ser Leu
 500 505 510
 Leu Leu Asp Cys Gly Glu Gly Thr Phe Gly Gln Leu Cys Arg His Tyr
 515 520 525
 Gly Asp Gln Val Asp Arg Val Leu Gly Thr Leu Ala Ala Val Phe Val
 530 535 540
 Ser His Leu His Ala Asp His His Thr Gly Leu Leu Asn Ile Leu Leu
 545 550 555 560
 Gln Arg Glu Gln Ala Leu Ala Ser Leu Gly Lys Pro Leu His Pro Leu
 565 570 575
 Leu Val Val Ala Pro Ser Gln Leu Lys Ala Trp Leu Gln Gln Tyr His
 580 585 590
 Asn Gln Cys Gln Glu Val Leu His His Ile Ser Met Ile Pro Ala Lys
 595 600 605
 Cys Leu Gln Glu Gly Ala Glu Ile Ser Ser Pro Ala Val Glu Arg Leu
 610 615 620
 Ile Ser Ser Leu Leu Arg Thr Cys Asp Leu Glu Glu Phe Gln Thr Cys
 625 630 635 640

Leu Val Arg His Cys Lys His Ala Phe Gly Cys Ala Leu Val His Thr
 645 650 655
 Ser Gly Trp Lys Val Val Tyr Ser Gly Asp Thr Met Pro Cys Glu Ala
 660 665 670
 Leu Val Arg Met Gly Lys Asp Ala Thr Leu Leu Ile His Glu Ala Thr
 675 680 685
 Leu Glu Asp Gly Leu Glu Glu Ala Val Glu Lys Thr His Ser Thr
 690 695 700
 Thr Ser Gln Ala Ile Ser Val Gly Met Arg Met Asn Ala Glu Phe Ile
 705 710 715 720
 Met Leu Asn His Phe Ser Gln Arg Tyr Ala Lys Val Pro Leu Phe Ser
 725 730 735
 Pro Asn Phe Asn Glu Lys Val Gly Val Ala Phe Asp His Met Lys Val
 740 745 750
 Cys Phe Gly Asp Phe Pro Thr Met Pro Lys Leu Ile Pro Pro Leu Lys
 755 760 765
 Ala Leu Phe Ala Gly Asp Ile Glu Glu Met Glu Glu Arg Arg Glu Lys
 770 775 780
 Arg Glu Leu Arg Gln Val Arg Ala Ala Leu Leu Ser Gly Glu Leu Ala
 785 790 795 800
 Gly Gly Leu Glu Asp Gly Glu Pro Gln Gln Lys Arg Ala His Thr Glu
 805 810 815
 Glu Pro Gln Ala Lys Lys Val Arg Ala Gln
 820 825

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 <211> 844
 <212> PRT
 <213> Caenorhabditis elegans

<400> 227
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 Ser Thr Ser Cys Leu Phe Lys Asp Asn Asn Glu Glu Leu Leu Glu Ser
 20 25 30
 Ile Lys Glu Arg Ile Ala Arg Asn Arg Arg Ile Leu Gln Lys His Ser
 35 40 45
 Ser Ser His Leu Lys Ala Arg Glu Val Asn Ala Ser Ile Ser Asn Leu
 50 55 60
 Arg Gln Ser Met Ala Ala Val Gln Lys Lys Gln Lys Ala Ala His Glu
 65 70 75 80
 Pro Pro Ala Asn Ser Ile Val Asn Ile Pro Ser Gln Val Ser Ile Glu
 85 90 95
 Val Leu Gly Asn Gly Thr Gly Leu Leu Arg Ala Cys Phe Ile Leu Arg
 100 105 110

Thr Pro Leu Lys Thr Tyr Met Phe Asn Cys Pro Glu Asn Ala Cys Arg
 115 120 125
 Phe Leu Trp Gln Leu Arg Ile Arg Ser Ser Ser Val Val Asp Leu Phe
 130 135 140
 Ile Thr Ser Ala Asn Trp Asp Asn Ile Ala Gly Ile Ser Ser Ile Leu
 145 150 155 160
 Leu Ser Lys Glu Ser Asn Ala Leu Ser Thr Arg Leu His Gly Ala Met
 165 170 175
 Asn Ile Lys His Phe Leu Glu Cys Ile Arg Pro Phe Gln Asp Ser Asp
 180 185 190
 Tyr Gly Ser Cys Lys Tyr Pro Ser Gln Val Glu Glu Arg Pro Tyr Thr
 195 200 205
 Met Glu Asn Tyr Glu Asp Ala Gly Leu Lys Val Thr Tyr Ile Pro Leu
 210 215 220
 Ser Pro Pro Leu Asn Ile Gly Ser Asn Asn Glu Lys Ser Lys Asn Val
 225 230 235 240
 Lys Val Asn Asn Val Asp Ile Ala Phe Leu Ile Glu Met Lys Glu Ala
 245 250 255
 Ala Arg Arg Ile Asp Thr Met Lys Leu Met Glu Leu Lys Val Pro Lys
 260 265 270
 Gly Pro Leu Ile Gly Lys Leu Lys Ser Gly Glu Ala Val Thr Leu Pro
 275 280 285
 Asp Gly Arg Thr Ile Gln Pro Asp Gln Val Phe Ser Ser Asp Lys Val
 290 295 300
 Glu Gly Asp Lys Pro Leu Leu Leu Val Thr Glu Cys Thr Thr Glu Asp
 305 310 315 320
 His Val Lys Ala Leu Ile Asp Ser Ser Ser Leu Gln Pro Phe Leu Asn
 325 330 335
 Gly Glu Lys Gln Leu Asp Tyr Met Val His Ile Ser Asp Asp Ala Val
 340 345 350
 Ile Asn Thr Pro Thr Tyr Arg His Leu Met Glu Lys Leu Asn Asn Pro
 355 360 365
 Ser Ile Thr His Leu Leu Ile Asn Gly Gly Asn Pro Val Ile Pro Ala
 370 375 380
 Val Glu Ser Val Tyr Lys His Thr Arg Leu Leu Arg Ser Ile Ala Pro
 385 390 395 400
 Ser Leu Phe Pro Ala Leu His Pro Ile Asp Trp Ser Gly Ile Ile Thr
 405 410 415
 Gln Asn Glu Glu Leu Ser Gln Arg Gln Asp Gln Phe Ile Arg Val Ala
 420 425 430
 Pro Met Gln Arg Tyr Trp Met Arg Arg Gly Ala Ser Phe Asn Glu Glu
 435 440 445

Pro Ile Val Asn Asn Leu Leu Ala Ala Glu Pro Glu Leu Ser Asp Lys
 450 455 460
 Ala Lys Glu Leu Ile Lys Glu Tyr Gln Lys Leu Glu Lys Glu Asn Lys
 465 470 475 480
 Met Asp Cys Glu Phe Pro Lys Leu Thr Phe Phe Gly Thr Ser Ser Ala
 485 490 495
 Val Pro Ser Lys Tyr Arg Asn Val Thr Gly Tyr Leu Val Glu Ala Ser
 500 505 510
 Glu Asn Ser Ala Ile Leu Ile Asp Val Gly Glu Gly Thr Tyr Gly Gln
 515 520 525
 Met Arg Ala Val Phe Gly Glu Asp Gly Cys Lys Gln Leu Leu Val Asn
 530 535 540
 Leu Asn Cys Val Leu Ile Thr His Ala His Gln Asp His Met Asn Gly
 545 550 555 560
 Leu Tyr Thr Ile Ile Ala Arg Arg Lys Glu Ala Phe Glu Ser Leu Gly
 565 570 575
 Ala Pro Tyr Arg Pro Leu Val Leu Val Cys Asn Arg Asn Val Leu Lys
 580 585 590
 Pro Met Lys Thr Tyr Ser Ile Cys Phe Glu Asn Ile Glu His Leu Leu
 595 600 605
 Glu Ile Val Asp Ile Ser Arg Tyr Pro Leu Thr Pro Pro Gly Ser Pro
 610 615 620
 Gly Gly Pro Pro Gly Lys Arg Pro Arg Leu Pro Ser Pro His Leu Pro
 625 630 635 640
 Pro Ser Arg Asp Val Leu Gln Asp Met Ser Ser Ser Phe Asp Lys Lys
 645 650 655
 Ala Trp Lys Leu Asp Glu Leu Lys Ala Val Gln Val His His Thr Arg
 660 665 670
 Met Ala Asn Gly Phe Val Met Arg Val Ala Gly Lys Arg Ile Val Phe
 675 680 685
 Ser Gly Asp Thr Lys Pro Cys Asp Leu Leu Val Glu Glu Gly Lys Asp
 690 695 700
 Ala Asp Val Leu Val His Glu Ser Thr Phe Glu Asp Gly His Glu Val
 705 710 715 720
 Asp Met Thr Pro Lys Pro Pro Lys Lys Leu Ala Lys Ile Ser Ser Leu
 725 730 735
 Ala Asp Ala Met Arg Lys Arg His Ser Thr Met Gly Gln Ala Val Asp
 740 745 750
 Val Gly Lys Arg Met Asn Ala Lys His Ile Ile Leu Thr His Phe Ser
 755 760 765
 Ala Arg Tyr Pro Lys Val Pro Val Leu Pro Glu Tyr Leu Asp Lys Glu
 770 775 780

Asn Ile Gly Val Ala Met Asp Met Leu Arg Val Arg Phe Asp His Leu
 785 790 795 800

Pro Leu Val Ser Lys Leu Leu Pro Ile Phe Arg Glu Val Phe Val Ala
 805 810 815

Glu Leu Phe Glu Leu Thr Ile Lys Lys Glu Gln Arg Val Leu Lys Asp
 820 825 830

Lys Glu Leu Ser Glu Lys Arg Gly Gln Leu Lys Ala
 835 840

<210> 228

<211> 837

<212> PRT

<213> Arabidopsis thaliana

<400> 228

Met Glu Asn Asn Glu Ala Thr Asn Gly Ser Lys Ser Ser Ser Asn Ser
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Phe Val Phe Asn Lys Arg Arg Ala Glu Gly Phe Asp Ile Thr Asp Lys
 20 25 30

Lys Lys Arg Asn Leu Glu Arg Lys Ser Gln Lys Leu Asn Pro Thr Asn
 35 40 45

Thr Ile Ala Tyr Ala Gln Ile Leu Gly Thr Gly Met Asp Thr Gln Asp
 50 55 60

Thr Ser Ser Ser Val Leu Leu Phe Phe Asp Lys Gln Arg Phe Ile Phe
 65 70 75 80

Asn Ala Gly Glu Gly Leu Gln Arg Phe Cys Thr Glu His Lys Ile Lys
 85 90 95

Leu Ser Lys Ile Asp His Val Phe Leu Ser Arg Val Cys Ser Glu Thr
 100 105 110

Ala Gly Gly Leu Pro Gly Leu Leu Thr Leu Ala Gly Ile Gly Glu
 115 120 125

Glu Gly Leu Ser Val Asn Val Trp Gly Pro Ser Asp Leu Asn Tyr Leu
 130 135 140

Val Asp Ala Met Lys Ser Phe Ile Pro Arg Ala Ala Met Val His Thr
 145 150 155 160

Arg Ser Phe Gly Pro Ser Ser Thr Pro Asp Pro Ile Val Leu Val Asn
 165 170 175

Asp Glu Val Val Lys Ile Ser Ala Ile Ile Leu Lys Pro Cys His Ser
 180 185 190

Glu Glu Asp Ser Gly Asn Lys Ser Gly Asp Leu Ser Val Val Tyr Val
 195 200 205

Cys Glu Leu Pro Glu Ile Leu Gly Lys Phe Asp Leu Glu Lys Ala Lys
 210 215 220

Lys Val Phe Gly Val Lys Pro Gly Pro Lys Tyr Ser Arg Leu Gln Ser
 225 230 235 240

Gly Glu Ser Val Lys Ser Asp Glu Arg Asp Ile Thr Val His Pro Ser
 245 250 255

Asp Val Met Gly Pro Ser Leu Pro Gly Pro Ile Val Leu Leu Val Asp
 260 265 270

Cys Pro Thr Glu Ser His Ala Ala Glu Leu Phe Ser Leu Lys Ser Leu
 275 280 285

Glu Ser Tyr Tyr Ser Ser Pro Asp Glu Gln Thr Ile Gly Ala Lys Phe
 290 295 300

Val Asn Cys Ile Ile His Leu Ser Pro Ser Ser Val Thr Ser Ser Pro
 305 310 315 320

Thr Tyr Gln Ser Trp Met Lys Lys Phe His Leu Thr Gln His Ile Leu
 325 330 335

Ala Gly His Gln Arg Phe Leu Pro Leu Leu Ile Ile Val Ser His Gln
 340 345 350

Lys Thr Val Arg Lys Asn Met Ala Phe Pro Ile Leu Lys Ala Ser Ser
 355 360 365

Arg Ile Ala Ala Arg Leu Asn Tyr Leu Cys Pro Gln Phe Phe Pro Ala
 370 375 380

Pro Gly Phe Trp Pro Ser Gln Leu Thr Asp Asn Ser Ile Ile Asp Pro
 385 390 395 400

Thr Pro Ser Asn Lys Phe Asn Leu Arg Pro Val Ala Ile Arg Gly Ile
 405 410 415

Asp Arg Ser Cys Ile Pro Ala Pro Leu Thr Ser Ser Glu Val Val Asp
 420 425 430

Glu Leu Leu Ser Glu Ile Pro Glu Ile Lys Asp Lys Ser Glu Glu Ile
 435 440 445

Lys Gln Phe Trp Asn Lys Gln His Asn Lys Thr Ile Ile Glu Lys Leu
 450 455 460

Trp Leu Ser Glu Cys Asn Thr Val Leu Pro Asn Cys Leu Glu Lys Ile
 465 470 475 480

Arg Arg Asp Asp Met Glu Ile Val Ile Leu Gly Thr Gly Ser Ser Gln
 485 490 495

Pro Ser Lys Tyr Arg Asn Val Ser Ala Ile Phe Ile Asp Leu Phe Ser
 500 505 510

Arg Gly Ser Leu Leu Leu Asp Cys Gly Glu Gly Thr Leu Gly Gln Leu
 515 520 525

Lys Arg Arg Tyr Gly Leu Asp Gly Ala Asp Glu Ala Val Arg Lys Leu
 530 535 540

Arg Cys Ile Trp Ile Ser His Ile His Ala Asp His His Thr Gly Leu
 545 550 555 560

Ala Arg Ile Leu Ala Leu Arg Ser Lys Leu Leu Lys Gly Val Thr His
 565 570 575

Glu Pro Val Ile Val Val Gly Pro Arg Pro Leu Lys Arg Phe Leu Asp
 580 585 590
 Ala Tyr Gln Arg Leu Glu Asp Leu Asp Met Glu Phe Leu Asp Cys Arg
 595 600 605
 Ser Thr Thr Ala Thr Ser Trp Ala Ser Leu Glu Ser Gly Gly Glu Ala
 610 615 620
 Glu Gly Ser Leu Phe Thr Gln Gly Ser Pro Met Gln Ser Val Phe Lys
 625 630 635 640
 Arg Ser Asp Ile Ser Met Asp Asn Ser Ser Val Leu Leu Cys Leu Lys
 645 650 655
 Asn Leu Lys Lys Val Leu Ser Glu Ile Gly Leu Asn Asp Leu Ile Ser
 660 665 670
 Phe Pro Val Val His Cys Pro Gln Ala Tyr Gly Val Val Ile Lys Ala
 675 680 685
 Ala Glu Arg Val Asn Ser Val Gly Glu Gln Ile Leu Gly Trp Lys Met
 690 695 700
 Val Tyr Ser Gly Asp Ser Arg Pro Cys Pro Glu Thr Val Glu Ala Ser
 705 710 715 720
 Arg Asp Ala Thr Ile Leu Ile His Glu Ala Thr Phe Glu Asp Ala Leu
 725 730 735
 Ile Glu Glu Ala Leu Ala Lys Asn His Ser Thr Thr Lys Glu Ala Ile
 740 745 750
 Asp Val Gly Ser Ala Ala Asn Val Tyr Arg Ile Val Leu Thr His Phe
 755 760 765
 Ser Gln Arg Tyr Pro Lys Ile Pro Val Ile Asp Glu Ser His Met His
 770 775 780
 Asn Thr Cys Ile Ala Phe Asp Leu Met Ser Ile Asn Met Ala Asp Leu
 785 790 795 800
 His Val Leu Pro Lys Val Leu Pro Tyr Phe Lys Thr Leu Phe Arg Asp
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 Glu Met Val Glu Asp Glu Asp Ala Asp Asp Val Ala Met Asp Asp Leu
 820 825 830
 Lys Glu Glu Ala Leu
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 20 25 30

Ser Arg Gly Thr Ser Met Cys Lys Ser Gln Glu Glu Pro Leu Asn Thr
 370 375 380
 Ile Ile Glu Lys Asp Asn Ile His Ile Phe Ser Gln Asn Lys Thr Val
 385 390 395 400
 Thr Phe Glu Pro Phe Arg Met Asn Glu Glu Pro Met Lys Cys Asn Ile
 405 410 415
 Asn Gly Glu Val Ala Asp Phe Ser Trp Gln Glu Ile Phe Glu Glu His
 420 425 430 435
 Val Lys Pro Leu Glu Phe Pro Leu Ala Asp Val Asp Thr Val Ile Asn
 435 440 445
 Asn Gln Leu His Val Asp Asn Phe Asn Asn Ser Ala Glu Lys Lys Lys
 450 455 460
 His Val Glu Ile Ile Thr Leu Gly Thr Gly Ser Ala Leu Pro Ser Lys
 465 470 475 480
 Tyr Arg Asn Val Val Ser Thr Leu Val Lys Val Pro Phe Thr Asp Ala
 485 490 495
 Asp Gly Asn Thr Ile Asn Arg Asn Ile Met Leu Asp Ala Gly Glu Asn
 500 505 510
 Thr Leu Gly Thr Ile His Arg Met Phe Ser Gln Leu Ala Val Lys Ser
 515 520 525
 Ile Phe Gln Asp Leu Lys Met Ile Tyr Leu Ser His Leu His Ala Asp
 530 535 540
 His His Leu Gly Ile Ile Ser Val Leu Asn Glu Trp Tyr Lys Tyr Asn
 545 550 555 560
 Lys Asp Asp Glu Thr Ser Tyr Ile Tyr Val Val Thr Pro Trp Gln Tyr
 565 570 575
 His Lys Phe Val Asn Glu Trp Leu Val Leu Glu Asn Lys Glu Ile Leu
 580 585 590
 Lys Arg Ile Lys Tyr Ile Ser Cys Glu His Phe Ile Asn Asp Ser Phe
 595 600 605
 Val Arg Met Gln Thr Gln Ser Val Pro Leu Ala Glu Phe Asn Glu Ile
 610 615 620
 Leu Lys Glu Asn Ser Asn Gln Glu Ser Asn Arg Lys Leu Glu Leu Asp
 625 630 635 640
 Arg Asp Ser Ser Tyr Arg Asp Val Asp Leu Ile Arg Gln Met Tyr Glu
 645 650 655
 Asp Leu Ser Ile Glu Tyr Phe Gln Thr Cys Arg Ala Ile His Cys Asp
 660 665 670 675
 Trp Ala Tyr Ser Asn Ser Ile Thr Phe Arg Met Asp Glu Asn Asn Glu
 675 680 685
 His Asn Thr Phe Lys Val Ser Tyr Ser Gly Asp Thr Arg Pro Asn Ile
 690 695 700

Glu Lys Phe Ser Leu Glu Ile Gly Tyr Asn Ser Asp Leu Leu Ile His
 705 710 715 720

Glu Ala Thr Leu Glu Asn Gln Leu Leu Glu Asp Ala Val Lys Lys Lys
 725 730 735

His Cys Thr Ile Asn Glu Ala Ile Gly Val Ser Asn Lys Met Asn Ala
 740 745 750

Arg Lys Leu Ile Leu Thr His Phe Ser Gln Arg Tyr Pro Lys Leu Pro
 755 760 765

Gln Leu Asp Asn Asn Ile Asp Val Met Ala Arg Glu Phe Cys Phe Ala
 770 775 780

Phe Asp Ser Met Ile Val Asp Tyr Glu Lys Ile Gly Glu Gln Gln Arg
 785 790 795 800

Ile Phe Pro Leu Leu Asn Lys Ala Phe Val Glu Glu Lys Glu Glu
 805 810 815

Glu Asp Val Asp Asp Val Glu Ser Val Gln Asp Leu Glu Val Lys Leu
 820 825 830

Lys Lys His Lys Lys Asn
 835

<210> 230
 <211> 311
 <212> PRT
 <213> Escherichia coli

<400> 230
 Met Lys Arg Asp Glu Leu Met Glu Leu Ile Phe Leu Gly Thr Ser Ala
 1 5 10 15

Gly Val Pro Thr Arg Thr Arg Asn Val Thr Ala Ile Leu Leu Asn Leu
 20 25 30

Gln His Pro Thr Gln Ser Gly Leu Trp Leu Phe Asp Cys Gly Glu Gly
 35 40 45

Thr Gln His Gln Leu Leu His Thr Ala Phe Asn Pro Gly Lys Leu Asp
 50 55 60

Lys Ile Phe Ile Ser His Leu His Gly Asp His Leu Phe Gly Leu Pro
 65 70 75 80

Gly Leu Leu Cys Ser Arg Ser Met Ser Gly Ile Ile Gln Pro Leu Thr
 85 90 95

Ile Tyr Gly Pro Gln Gly Ile Arg Glu Phe Val Glu Thr Ala Leu Arg
 100 105 110

Ile Ser Gly Ser Trp Thr Asp Tyr Pro Leu Glu Ile Val Glu Ile Gly
 115 120 125

Ala Gly Glu Ile Leu Asp Asp Gly Leu Arg Lys Val Thr Ala Tyr Pro
 130 135 140

Leu Glu His Pro Leu Glu Cys Tyr Gly Tyr Arg Ile Glu Glu His Asp
 145 150 155 160

Lys Pro Gly Ala Leu Asn Ala Gln Ala Leu Lys Ala Ala Gly Val Pro
 165 170 175
 Pro Gly Pro Leu Phe Gln Glu Leu Lys Ala Gly Lys Thr Ile Thr Leu
 180 185 190
 Glu Asp Gly Arg Gln Ile Asn Gly Ala Asp Tyr Leu Ala Ala Pro Val
 195 200 205
 Pro Gly Lys Ala Leu Ala Ile Phe Gly Asp Thr Gly Pro Cys Asp Ala
 210 215 220
 Ala Leu Asp Leu Ala Lys Gly Val Asp Val Met Val His Glu Ala Thr
 225 230 235 240
 Leu Asp Ile Thr Met Glu Ala Lys Ala Asn Ser Arg Gly His Ser Ser
 245 250 255
 Thr Arg Gln Ala Ala Thr Leu Ala Arg Glu Ala Gly Val Gly Lys Leu
 260 265 270
 Ile Ile Thr His Val Ser Ser Arg Tyr Asp Asp Lys Gly Cys Gln His
 275 280 285
 Leu Leu Arg Glu Cys Arg Ser Ile Phe Pro Ala Thr Glu Leu Ala Asn
 290 295 300
 Asp Phe Thr Val Phe Asn Val
 305 310
 <210> 231
 <211> 326
 <212> PRT
 <213> Synechocystis sp.
 <400> 231
 Met Glu Ile Thr Phe Leu Gly Thr Ser Ser Gly Val Pro Thr Arg Asn
 1 5 10 15
 Arg Asn Val Ser Ser Ile Ala Leu Arg Leu Pro Gln Arg Ala Glu Leu
 20 25 30
 Trp Leu Phe Asp Cys Gly Glu Gly Thr Gln His Gln Phe Leu Arg Ser
 35 40 45
 Glu Val Lys Ile Ser Gln Leu Thr Arg Ile Phe Ile Thr His Leu His
 50 55 60
 Gly Asp His Ile Phe Gly Leu Met Gly Leu Leu Ala Ser Ser Gly Leu
 65 70 75 80
 Ala Gly Ser Gly Gln Gly Ile Glu Ile Tyr Gly Pro Glu Gly Leu Gly
 85 90 95
 Asp Tyr Leu Glu Ala Cys Cys Arg Phe Ser Ser Thr His Leu Gly Lys
 100 105 110
 Arg Leu Lys Val His Thr Val Arg Glu Asn Gly Leu Ile Tyr Glu Asp
 115 120 125
 Lys Asp Phe Gln Val His Cys Gly Leu Leu Lys His Arg Ile Pro Ala
 130 135 140

Tyr Gly Tyr Arg Val Glu Glu Lys Gln Arg Pro Gly Arg Phe Asn Val
 145 150 155 160
 Glu Gln Ala Glu Ala Leu Gly Ile Pro Phe Gly Pro Ile Tyr Gly Gln
 165 170 175
 Leu Lys Gln Gly Lys Thr Val Thr Leu Glu Asp Gly Arg Arg Ile Arg
 180 185 190
 Gly Gln Asp Leu Cys Glu Pro Pro Glu Pro Gly Arg Lys Phe Val Tyr
 195 200 205
 Cys Thr Asp Thr Val Phe Cys Glu Ala Ile Ala Leu Ala Gln Glu
 210 215 220
 Ala Asp Leu Leu Val His Glu Ala Thr Phe Ala His Gln Asp Ala Gln
 225 230 235 240
 Leu Ala Phe Asp Arg Leu His Ser Thr Ser Thr Met Ala Ala Gln Val
 245 250 255
 Ala Leu Leu Ala Asn Val Lys Gln Leu Ile Met Thr His Phe Ser Pro
 260 265 270
 Arg Tyr Ala Pro Gly Asn Pro Leu Gln Leu Glu Asn Leu Leu Ala Glu
 275 280 285
 Ala Gln Ala Ile Phe Pro Asn Thr Arg Leu Ala Arg Asp Phe Leu Thr
 290 295 300
 Val Glu Ile Pro Arg Arg Thr Ala Asp Pro Ala Ile Ala Met Ser Thr
 305 310 315 320
 Pro Gln Ala Ser Pro Ala
 325

<210> 232
 <211> 307
 <212> PRT
 <213> Methanobacterium thermoautotrophicum
 <400> 232
 Met Met Glu Val Thr Phe Leu Gly Thr Ser Ser Ala Val Pro Ser Lys
 1 5 10 15
 Asn Arg Asn His Thr Ser Ile Ala Leu Arg Ile Pro Gly Glu Ile Phe
 20 25 30
 Leu Phe Asp Cys Gly Glu Gly Thr Gln Arg Gln Met Ala Leu Ala Gly
 35 40 45
 Ile Ser Pro Met Lys Val Thr Arg Ile Phe Ile Thr His Leu His Gly
 50 55 60
 Asp His Ile Leu Gly Ile Pro Gly Met Ile Gln Ser Met Gly Phe Arg
 65 70 75 80
 Gly Arg Glu Glu Pro Leu Asp Ile Tyr Gly Pro Pro Gly Ile His Glu
 85 90 95
 Leu His Glu Cys Ile Met Lys Met Gln Tyr Phe Thr Leu Asp Phe Asp
 100 105 110

DODDLE/2001

Ile Asn Val His Glu Val Arg Gly Gly Thr Val Val Glu Glu Asp Asp
 115 120 125

Tyr Arg Val Thr Ser Ala Pro Ala Ser His Ser Val Phe Asn Leu Ala
 130 135 140

Tyr Cys Phe Glu Glu Lys Lys Arg Pro Arg Phe Leu Arg Glu Lys Ala
 145 150 155 160

Ile Ala Leu Gly Leu Lys Pro Gly Pro Ala Phe Gly Lys Leu His Arg
 165 170 175

Gly Ile Pro Val Arg Val Gly Asp Arg Ile Ile Met Pro Glu Glu Val
 180 185 190

Leu Gly Ser Pro Arg Lys Gly Val Lys Val Cys Tyr Ser Gly Asp Thr
 195 200 205

Arg Pro Cys Glu Ser Val Ile Lys Leu Ala Glu Gly Ala Glu Leu Leu
 210 215 220

Ile His Glu Ser Thr Leu Glu Ala Gly Ser Glu Asp Lys Ala Ala Glu
 225 230 235 240

Ser Gly His Ser Thr Ala Arg Glu Ala Ala Glu Val Ala Arg Ser Ala
 245 250 255

Gly Val Lys Arg Leu Ile Leu Thr His Leu Ser Thr Arg Tyr Lys Arg
 260 265 270

Thr Glu Val Ile Leu Glu Ala Ala Arg Gln Val Phe Pro Val Thr Asp
 275 280 285

Val Ala Asp Asp Leu Met Thr Val Glu Val Lys Ala Tyr Asp Ser Ser
 290 295 300

Pro Asp Ser
 305

<210> 233
<211> 684
<212> PRT
<213> Homo sapiens

<400> 233
Met Ser Ala Ile Pro Ala Glu Glu Ser Asp Gln Leu Leu Ile Arg Pro
 1 5 10 15

Leu Gly Ala Gly Gln Glu Val Gly Arg Ser Cys Ile Ile Leu Glu Phe
 20 25 30

Lys Gly Arg Lys Ile Met Leu Asp Cys Gly Ile His Pro Gly Leu Glu
 35 40 45

Gly Met Asp Ala Leu Pro Tyr Ile Asp Leu Ile Asp Pro Ala Glu Ile
 50 55 60

Asp Leu Leu Leu Ile Ser His Phe His Leu Asp His Cys Gly Ala Leu
 65 70 75 80

Pro Trp Phe Leu Gln Lys Thr Ser Phe Lys Gly Arg Thr Phe Met Thr
 85 90 95

His Ala Thr Lys Ala Ile Tyr Arg Trp Leu Leu Ser Asp Tyr Val Lys
 100 105 110
 Val Ser Asn Ile Ser Ala Asp Asp Met Leu Tyr Thr Glu Thr Asp Leu
 115 120 125
 Glu Glu Ser Met Asp Lys Ile Glu Thr Ile Asn Phe His Glu Val Lys
 130 135 140
 Glu Val Ala Gly Ile Lys Phe Trp Cys Tyr His Ala Gly His Val Leu
 145 150 155 160
 Gly Ala Ala Met Phe Met Ile Glu Ile Ala Gly Val Lys Leu Leu Tyr
 165 170 175
 Thr Gly Asp Phe Ser Arg Gln Glu Asp Arg His Leu Met Ala Ala Glu
 180 185 190
 Ile Pro Asn Ile Lys Pro Asp Ile Leu Ile Ile Glu Ser Thr Tyr Gly
 195 200 205
 Thr His Ile His Glu Lys Arg Glu Glu Arg Glu Ala Arg Phe Cys Asn
 210 215 220
 Thr Val His Asp Ile Val Asn Arg Gly Gly Arg Gly Leu Ile Pro Val
 225 230 235 240
 Phe Ala Leu Gly Arg Ala Gln Glu Leu Leu Ile Leu Asp Glu Tyr
 245 250 255
 Trp Gln Asn His Pro Glu Leu His Asp Ile Pro Ile Tyr Tyr Ala Ser
 260 265 270
 Ser Leu Ala Lys Lys Cys Met Ala Val Tyr Gln Thr Tyr Val Asn Ala
 275 280 285
 Met Asn Asp Lys Ile Arg Lys Gln Ile Asn Ile Asn Asn Pro Phe Val
 290 295 300
 Phe Lys His Ile Ser Asn Leu Lys Ser Met Asp His Phe Asp Asp Ile
 305 310 315 320
 Gly Pro Ser Val Val Met Ala Ser Pro Gly Met Met Gln Ser Gly Leu
 325 330 335
 Ser Arg Glu Leu Phe Glu Ser Trp Cys Thr Asp Lys Arg Asn Gly Val
 340 345 350
 Ile Ile Ala Gly Tyr Cys Val Glu Gly Thr Leu Ala Lys His Ile Met
 355 360 365
 Ser Glu Pro Glu Glu Ile Thr Thr Met Ser Gly Gln Lys Leu Pro Leu
 370 375 380
 Lys Met Ser Val Asp Tyr Ile Ser Phe Ser Ala His Thr Asp Tyr Gln
 385 390 395 400
 Gln Thr Ser Glu Phe Ile Arg Ala Leu Lys Pro Pro His Val Ile Leu
 405 410 415
 Val His Gly Glu Gln Asn Glu Met Ala Arg Leu Lys Ala Ala Leu Ile
 420 425 430

Arg Glu Tyr Glu Asp Asn Asp Glu Val His Ile Glu Val His Asn Pro
 435 440 445
 Arg Asn Thr Glu Ala Val Thr Leu Asn Phe Arg Gly Glu Lys Leu Ala
 450 455 460
 Lys Val Met Gly Phe Leu Ala Asp Lys Pro Glu Gln Gly Gln Arg
 465 470 475 480
 Val Ser Gly Ile Leu Val Lys Arg Asn Phe Asn Tyr His Ile Leu Ser
 485 490 495
 Pro Cys Asp Leu Ser Asn Tyr Thr Asp Leu Ala Met Ser Thr Val Lys
 500 505 510
 Gln Thr Gln Ala Ile Pro Tyr Thr Gly Pro Phe Asn Leu Leu Cys Tyr
 515 520 525
 Gln Leu Gln Lys Leu Thr Gly Asp Val Glu Glu Leu Glu Ile Gln Glu
 530 535 540
 Lys Pro Ala Leu Lys Val Phe Lys Asn Ile Thr Val Ile Gln Glu Pro
 545 550 555 560
 Gly Met Val Val Leu Glu Trp Leu Ala Asn Pro Ser Asn Asp Met Tyr
 565 570 575
 Ala Asp Thr Val Thr Val Ile Leu Glu Val Gln Ser Asn Pro Lys
 580 585 590
 Ile Arg Lys Gly Ala Val Gln Lys Val Ser Lys Lys Leu Glu Met His
 595 600 605
 Val Tyr Ser Lys Arg Leu Glu Ile Met Leu Gln Asp Ile Phe Gly Glu
 610 615 620
 Asp Cys Val Ser Val Lys Asp Asp Ser Ile Leu Ser Val Thr Val Asp
 625 630 635 640
 Gly Lys Thr Ala Asn Leu Asn Leu Glu Thr Arg Thr Val Glu Cys Glu
 645 650 655
 Glu Gly Ser Glu Asp Asp Glu Ser Leu Arg Glu Met Val Glu Leu Ala
 660 665 670
 Ala Gln Arg Leu Tyr Glu Ala Leu Thr Pro Val His
 675 680

 <210> 234
 <211> 693
 <212> PRT
 <213> *Arabidopsis thaliana*

 <400> 234
 Met Ala Ser Ser Ser Thr Ser Leu Lys Arg Arg Glu Gln Pro Ile Ser
 1 5 10 15
 Arg Asp Gly Asp Gln Leu Ile Val Thr Pro Leu Gly Ala Gly Ser Glu
 20 25 30
 Val Gly Arg Ser Cys Val Tyr Met Ser Phe Arg Gly Lys Asn Ile Leu
 35 40 45

Phe Asp Cys Gly Ile His Pro Ala Tyr Ser Gly Met Ala Ala Leu Pro
 50 55 60
 Tyr Phe Asp Glu Ile Asp Pro Ser Ser Ile Asp Val Leu Leu Ile Thr
 65 70 75 80
 His Phe His Ile Asp His Ala Ala Ser Leu Pro Tyr Phe Leu Glu Lys
 85 90 95
 Thr Thr Phe Asn Gly Arg Val Phe Met Thr His Ala Thr Lys Ala Ile
 100 105 110
 Tyr Lys Leu Leu Leu Thr Asp Tyr Val Lys Val Ser Lys Val Ser Val
 115 120 125
 Glu Asp Met Leu Phe Asp Glu Gln Asp Ile Asn Lys Ser Met Asp Lys
 130 135 140
 Ile Glu Val Ile Asp Phe His Gln Thr Val Glu Val Asn Gly Ile Lys
 145 150 155 160
 Phe Trp Cys Tyr Thr Ala Gly His Val Leu Gly Ala Ala Met Phe Met
 165 170 175
 Val Asp Ile Ala Gly Val Arg Ile Leu Tyr Thr Gly Asp Tyr Ser Arg
 180 185 190
 Glu Glu Asp Arg His Leu Arg Ala Ala Glu Leu Pro Gln Phe Ser Pro
 195 200 205
 Asp Ile Cys Ile Ile Glu Ser Thr Ser Gly Val Gln Leu His Gln Ser
 210 215 220
 Arg His Ile Arg Glu Lys Arg Phe Thr Asp Val Ile His Ser Thr Val
 225 230 235 240
 Ala Gln Gly Arg Val Leu Ile Pro Ala Phe Ala Leu Gly Arg Ala
 245 250 255
 Gln Glu Leu Leu Ile Leu Asp Glu Tyr Trp Ala Asn His Pro Asp
 260 265 270
 Leu His Asn Ile Pro Ile Tyr Tyr Ala Ser Pro Leu Ala Lys Lys Cys
 275 280 285
 Met Ala Val Tyr Gln Thr Tyr Ile Leu Ser Met Asn Asp Arg Ile Arg
 290 295 300
 Asn Gln Phe Ala Asn Ser Asn Pro Phe Val Phe Lys His Ile Ser Pro
 305 310 315 320
 Leu Asn Ser Ile Asp Asp Phe Asn Asp Val Gly Pro Ser Val Val Met
 325 330 335
 Ala Thr Pro Gly Gly Leu Gln Ser Gly Leu Ser Arg Gln Leu Phe Asp
 340 345 350 355
 Ser Trp Cys Ser Asp Lys Lys Asn Ala Cys Ile Ile Pro Gly Tyr Met
 355 360 365
 Val Glu Gly Thr Leu Ala Lys Thr Ile Ile Asn Glu Pro Lys Glu Val
 370 375 380

Thr Leu Met Asn Gly Leu Thr Ala Pro Leu Asn Met Gln Val His Tyr
 385 390 395 400
 Ile Ser Phe Ser Ala His Ala Asp Tyr Ala Gln Thr Ser Thr Phe Leu
 405 410 415
 Lys Glu Leu Met Pro Pro Asn Ile Ile Leu Val His Gly Glu Ala Asn
 420 425 430
 Glu Met Met Arg Leu Lys Gln Lys Leu Leu Thr Glu Phe Pro Asp Gly
 435 440 445
 Asn Thr Lys Ile Met Thr Pro Lys Asn Cys Glu Ser Val Glu Met Tyr
 450 455 460
 Phe Asn Ser Glu Lys Leu Ala Lys Thr Ile Gly Arg Leu Ala Glu Lys
 465 470 475 480
 Thr Pro Asp Val Gly Asp Thr Val Ser Gly Ile Leu Val Lys Lys Gly
 485 490 495
 Phe Thr Tyr Gln Ile Met Ala Pro Asp Glu Leu His Val Phe Ser Gln
 500 505 510
 Leu Ser Thr Ala Thr Val Thr Gln Arg Ile Thr Ile Pro Phe Val Gly
 515 520 525
 Ala Phe Gly Val Ile Lys His Arg Leu Glu Lys Ile Phe Glu Ser Val
 530 535 540
 Glu Phe Ser Thr Asp Glu Glu Ser Gly Leu Pro Ala Leu Lys Val His
 545 550 555 560
 Glu Arg Val Thr Val Lys Gln Glu Ser Glu Lys His Ile Ser Leu Gln
 565 570 575
 Trp Ser Ser Asp Pro Ile Ser Asp Met Val Ser Asp Ser Ile Val Ala
 580 585 590
 Leu Ile Leu Asn Ile Ser Arg Glu Val Pro Lys Ile Val Met Glu Glu
 595 600 605
 Glu Asp Ala Val Lys Ser Glu Glu Glu Asn Gly Lys Lys Val Glu Lys
 610 615 620
 Val Ile Tyr Ala Leu Leu Val Ser Leu Phe Gly Asp Val Lys Leu Gly
 625 630 635 640
 Glu Asn Gly Lys Leu Val Ile Arg Val Asp Gly Asn Val Ala Gln Leu
 645 650 655
 Asp Lys Glu Ser Gly Glu Val Glu Ser Glu His Ser Gly Leu Lys Glu
 660 665 670
 Arg Val Arg Val Ala Phe Glu Arg Ile Gln Ser Ala Val Lys Pro Ile
 675 680 685
 Pro Leu Ser Ala Ser
 690

<210> 235

<211> 779

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 235

Met	Glu	Arg	Thr	Asn	Thr	Thr	Phe	Lys	Phe	Ser	Leu	Gly	Gly
1				5				10			15		

Ser	Asn	Glu	Val	Gly	Arg	Ser	Cys	His	Ile	Leu	Gln	Tyr	Lys	Gly	Lys
		20					25					30			

Thr	Val	Met	Leu	Asp	Ala	Gly	Ile	His	Pro	Ala	Tyr	Gln	Gly	Leu	Ala
		35					40					45			

Ser	Leu	Pro	Phe	Tyr	Asp	Glu	Phe	Asp	Leu	Ser	Lys	Val	Asp	Ile	Leu
		50				55					60				

Leu	Ile	Ser	His	Phe	His	Leu	Asp	His	Ala	Ala	Ser	Leu	Pro	Tyr	Val
	65				70				75				80		

Met	Gln	Arg	Thr	Asn	Phe	Gln	Gly	Arg	Val	Phe	Met	Thr	His	Pro	Thr
	85							90				95			

Lys	Ala	Ile	Tyr	Arg	Trp	Leu	Leu	Arg	Asp	Phe	Val	Arg	Val	Thr	Ser
	100						105					110			

Ile	Gly	Ser	Ser	Ser	Ser	Met	Gly	Thr	Lys	Asp	Glu	Gly	Leu	Phe
	115					120					125			

Ser	Asp	Glu	Asp	Leu	Val	Asp	Ser	Phe	Asp	Lys	Ile	Glu	Thr	Val	Asp
	130					135					140				

Tyr	His	Ser	Thr	Val	Asp	Val	Asn	Gly	Ile	Lys	Phe	Thr	Ala	Phe	His
	145					150				155			160		

Ala	Gly	His	Val	Leu	Gly	Ala	Ala	Met	Phe	Gln	Ile	Glu	Ile	Ala	Gly
	165									170			175		

Leu	Arg	Val	Leu	Phe	Thr	Gly	Asp	Tyr	Ser	Arg	Glu	Val	Asp	Arg	His
	180						185					190			

Leu	Asn	Ser	Ala	Glu	Val	Pro	Leu	Ser	Ser	Asn	Val	Leu	Ile	Val
	195						200					205		

Glu	Ser	Thr	Phe	Gly	Thr	Ala	Thr	His	Glu	Pro	Arg	Leu	Asn	Arg	Glu
	210						215					220			

Arg	Lys	Leu	Thr	Gln	Leu	Ile	His	Ser	Thr	Val	Met	Arg	Gly	Gly	Arg
	225						230			235			240		

Val	Leu	Leu	Pro	Val	Phe	Ala	Leu	Gly	Arg	Ala	Gln	Glu	Ile	Met	Leu
							245			250			255		

Ile	Leu	Asp	Glu	Tyr	Trp	Ser	Gln	His	Ala	Asp	Glu	Leu	Gly	Gly	Gly
		260					265					270			

Gln	Val	Pro	Ile	Phe	Tyr	Ala	Ser	Asn	Leu	Ala	Lys	Lys	Cys	Met	Ser
		275					280					285			

Val	Phe	Gln	Thr	Tyr	Val	Asn	Met	Met	Asn	Asp	Ile	Arg	Lys	Lys	
		290					295					300			

Phe Arg Asp Ser Gln Thr Asn Pro Phe Ile Phe Lys Asn Ile Ser Tyr
 305 310 315 320

Leu Arg Asn Leu Glu Asp Phe Gln Asp Phe Gly Pro Ser Val Met Leu
 325 330 335

Ala Ser Pro Gly Met Leu Gln Ser Gly Leu Ser Arg Asp Leu Leu Glu
 340 345 350

Arg Trp Cys Pro Glu Asp Lys Asn Leu Val Leu Ile Thr Gly Tyr Ser
 355 360 365

Ile Glu Gly Thr Met Ala Lys Phe Ile Met Leu Glu Pro Asp Thr Ile
 370 375 380

Pro Ser Ile Asn Asn Pro Glu Ile Thr Ile Pro Arg Arg Cys Gln Val
 385 390 395 400

Glu Glu Ile Ser Phe Ala Ala His Val Asp Phe Gln Glu Asn Leu Glu
 405 410 415

Phe Ile Glu Lys Ile Ser Ala Pro Asn Ile Ile Leu Val His Gly Glu
 420 425 430

Ala Asn Pro Met Gly Arg Leu Lys Ser Ala Leu Leu Ser Asn Phe Ala
 435 440 445

Ser Leu Lys Gly Thr Asp Asn Glu Val His Val Phe Asn Pro Arg Asn
 450 455 460

Cys Val Glu Val Asp Leu Glu Phe Gln Gly Val Lys Val Ala Lys Ala
 465 470 475 480

Val Gly Asn Ile Val Asn Glu Ile Tyr Lys Glu Glu Asn Val Glu Ile
 485 490 495

Lys Glu Glu Ile Ala Ala Lys Ile Glu Pro Ile Lys Glu Glu Asn Glu
 500 505 510

Asp Asn Leu Asp Ser Gln Ala Glu Lys Gly Leu Val Asp Glu Glu Glu
 515 520 525

His Lys Asp Ile Val Val Ser Gly Ile Leu Val Ser Asp Asp Lys Asn
 530 535 540

Phe Glu Leu Asp Phe Leu Ser Leu Ser Asp Leu Arg Glu His His Pro
 545 550 555 560

Asp Leu Ser Thr Thr Ile Leu Arg Glu Arg Gln Ser Val Arg Val Asn
 565 570 575

Cys Lys Lys Glu Leu Ile Tyr Trp His Ile Leu Gln Met Phe Gly Glu
 580 585 590

Ala Glu Val Leu Gln Asp Asp Asp Arg Val Thr Asn Gln Glu Pro Lys
 595 600 605

Val Lys Glu Glu Ser Lys Asp Asn Leu Thr Asn Thr Gly Lys Leu Ile
 610 615 620

Leu Gln Ile Met Gly Asp Ile Lys Leu Thr Ile Val Asn Thr Leu Ala
 625 630 635 640

Val Val Glu Trp Thr Gln Asp Leu Met Asn Asp Thr Val Ala Asp Ser
 645 650 655
 Ile Ile Ala Ile Leu Met Asn Val Asp Ser Ala Pro Ala Ser Val Lys
 660 665 670
 Leu Ser Ser His Ser Cys Asp Asp His Asp His Asn Asn Val Gln Ser
 675 680 685
 Asn Ala Gln Gly Lys Ile Asp Glu Val Glu Arg Val Lys Gln Ile Ser
 690 695 700
 Arg Leu Phe Lys Glu Gln Phe Gly Asp Cys Phe Thr Leu Phe Leu Asn
 705 710 715 720
 Lys Asp Glu Tyr Ala Ser Asn Lys Glu Glu Thr Ile Thr Gly Val Val
 725 730 735
 Thr Ile Gly Lys Ser Thr Ala Lys Ile Asp Phe Asn Asn Met Lys Ile
 740 745 750
 Leu Glu Cys Asn Ser Asn Pro Leu Lys Gly Arg Val Glu Ser Leu Leu
 755 760 765
 Asn Ile Gly Gly Asn Leu Val Thr Pro Leu Cys
 770 775

<210> 236
 <211> 554
 <212> FRT
 <213> Synechocystis sp.

<400> 236
 Met Thr Phe Ser Val Pro Thr Gln Gly Lys Ala Phe Ala Asn Ile Ser
 1 5 10 15
 Phe Leu Pro Tyr Gly Val Gly Pro Arg Asp Gly Gly Ile Cys Leu Glu
 20 25 30
 Leu His Leu Gly Pro Tyr Arg Ile Leu Leu Asp Cys Gly Leu Glu Asp
 35 40 45
 Leu Thr Pro Leu Leu Ala Ala Asp Pro Gly Thr Val Asp Leu Val Phe
 50 55 60
 Cys Ser His Ala His Arg Asp His Gly Leu Gly Leu Trp Gln Phe His
 65 70 75 80
 Gln Gln Phe Pro His Ile Pro Ile Leu Ala Ser Glu Val Thr Gln Arg
 85 90 95
 Leu Leu Pro Leu Asn Trp Pro Asp Glu Phe Val Pro Pro Phe Cys Arg
 100 105 110
 Val Leu Pro Trp Arg Ser Pro Gln Glu Val Leu Pro Gly Leu Thr Val
 115 120 125
 Glu Leu Leu Pro Ala Gly His Leu Pro Gly Ala Ala Leu Ile Leu Leu
 130 135 140
 Glu Tyr His Asn Gly Asp Arg Leu Tyr Arg Val Ile Tyr Thr Gly Asp
 145 150 155 160

Tyr Cys Leu Ser His Leu Gln Leu Val Asp Gly Leu Ala Leu Thr Pro
 165 170 175
 Leu Arg Gly Leu Lys Pro Asp Val Leu Ile Leu Glu Gly His Tyr Gly
 180 185 190
 Asn Arg Arg Leu Pro His Arg Arg Gln Gln Glu Lys Gln Phe Ile Gln
 195 200 205
 Ala Ile Glu Thr Val Leu Ala Lys Gly Arg Asn Ile Leu Leu Pro Val
 210 215 220
 Pro Pro Leu Gly Leu Ala Gln Glu Ile Leu Lys Leu Leu Arg Thr His
 225 230 235 240
 His Gln Phe Thr Gly Arg Gln Val Asn Leu Trp Ala Gly Glu Ser Val
 245 250 255
 Ala Arg Gly Cys Asp Ala Tyr Gln Gly Ile Ile Asp His Leu Pro Asp
 260 265 270
 Asn Val Arg Asn Phe Ala Gln His Gln Pro Leu Phe Trp Asp Asp Lys
 275 280 285
 Val Tyr Pro His Leu Arg Pro Leu Thr Asp Asp Gln Gly Glu Leu Ser
 290 295 300
 Leu Ser Ala Pro Ser Ile Val Ile Thr Thr Thr Trp Pro Ala Phe Trp
 305 310 315 320
 Pro Ser Pro Ala Ala Leu Pro Gly Leu Trp Thr Val Phe Met Pro Gln
 325 330 335
 Leu Leu Thr Leu Pro Ser Cys Leu Val Asn Phe Ala Trp Gln Asp Leu
 340 345 350
 Glu Glu Phe Pro Lys Tyr Glu Leu Glu Asp Tyr Leu Leu Ala Asp His
 355 360 365
 Ser Asp Gly Arg Asn Thr Thr Gln Leu Ile His Asn Leu Arg Pro Gln
 370 375 380
 His Leu Val Phe Val His Gly Gln Pro Ser Asp Ile Glu Asp Leu Thr
 385 390 395 400
 Ser Leu Glu Glu Leu Gln Ser Arg Tyr Gln Leu His Ser Pro Ala Ala
 405 410 415
 Gly Asn Ala Val Ala Leu Pro Ile Gly Asp Arg Phe Val Gln Pro Thr
 420 425 430
 Pro Pro Pro Gln Ile Tyr Glu Gly Glu Ile His Glu Leu Glu Pro
 435 440 445
 Asn Lys Gln Ile His His Leu Gly Glu Val Val Ile His Leu Asp Gly
 450 455 460
 Gln Ile Leu Glu Asn Ser Arg Trp Gly Lys Phe Gly Glu Thr Gly Ile
 465 470 475 480
 Val Gln Ala Arg Trp Gln Gly Glu Glu Leu Val Leu Arg Gly Ile Ser
 485 490 495

 0
666667
8886687
- 1112222111

Gln Arg Glu Leu Leu Lys Gln Asn Gln Ser Ser Lys Arg Pro Val Asp
500 505 510

Phe Asp Cys Cys Ala Asn Cys Arg His Phe Gln His Tyr His Cys Arg
515 520 525

Asn Pro Val Ser Pro Leu Met Gly Leu Glu Val Arg Ala Asp Gly His
530 535 540

Cys Pro Val Phe Glu Ser Val Ala Ser Ser
545 550

<210> 237

<211> 636

<212> PRT

<213> Methanobacterium thermoautotrophicum

```

<400> 237
Met Val Ser Glu Met Leu Glu Glu Ile Lys Arg Thr Ile Met Gln Arg
      1           5           10          15

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Leu Pro Glu Arg Val Gln Val Ala Lys Val Glu Phe Glu Gly Pro Glu
20 25 30

Val Val Ile Tyr Thr Lys Asn Pro Glu Ile Ile Thr Glu Asn Gly Asn
35 40 45

Leu Ile Arg Asp Ile Ala Lys Asp Ile Arg Lys Arg Ile Ile Ile Arg
50 55 60

Ser Asp Arg Ser Val Leu Met Asp Pro Glu Lys Ala Ile Arg Lys Ile
65 70 75 80

His Glu Ile Val Pro Glu Glu Ala Lys Ile Thr Asn Ile Ser Phe Asp
85 90 95

Asp Val Thr Cys Glu Val Ile Ile Glu Ala Arg Lys Pro Gly Leu Val
100 105 110

Ile Gly Lys Tyr Gly Ser Thr Ser Arg Glu Ile Val Lys Asn Thr Gly
115 120 125

Trp Ala Pro Lys Ile Leu Arg Thr Pro Pro Pro Ile Ser Ser Glu Ile Ile
130 135 140

Glu Arg Ile Arg Arg Thr Leu Arg Lys Asn Ser Lys Glu Arg Lys Lys
145 150 155 160

Ile Leu Gln Gln Leu Gly Asn Arg Ile His Gln Lys Pro Lys Tyr Asp
165 170 175

Asn Asp Trp Ala Arg Leu Thr Ala Met Gly Gly Phe Arg Glu Val Gly
180 185 190

Arg Ser Cys Leu Tyr Leu Gln Thr Pro Asn Ser Arg Val Leu Leu Asp
195 200 205

Cys Gly Val Asn Val Ala Gly Gly Asp Asp Lys Asn Ser Tyr Pro Tyr
210 215 220

Leu Asn Val Pro Glu Phe Thr Leu Asp Ser Leu Asp Ala Val Ile Ile
225 230 235 240

Thr His Ala His Leu Asp His Ser Gly Phe Leu Pro Tyr Leu Tyr His
 245 250 255
 Tyr Gly Tyr Asp Gly Pro Val Tyr Cys Thr Ala Pro Thr Arg Asp Leu
 260 265 270
 Met Thr Leu Leu Gln Leu Asp His Ile Asp Ile Ala His Arg Glu Asp
 275 280 285
 Glu Pro Leu Pro Phe Asn Val Lys His Val Lys Lys Ser Val Lys His
 290 295 300
 Thr Ile Thr Leu Asp Tyr Gly Glu Val Thr Asp Ile Ala Pro Asp Ile
 305 310 315 320
 Arg Leu Thr Leu His Asn Ala Gly His Ile Leu Gly Ser Ala Met Ala
 325 330 335
 His Leu His Ile Gly Asp Gly Gln His Asn Met Val Tyr Thr Gly Asp
 340 345 350
 Phe Lys Tyr Glu Gln Ser Arg Leu Leu Glu Ala Ala Ala Asn Arg Phe
 355 360 365
 Pro Arg Ile Glu Thr Leu Val Met Glu Ser Thr Tyr Gly Gly His Glu
 370 375 380
 Asp Val Gln Pro Ser Arg Asn Arg Ala Glu Lys Glu Leu Val Lys Thr
 385 390 395 400
 Ile Tyr Ser Thr Leu Arg Arg Gly Gly Lys Ile Leu Ile Pro Val Phe
 405 410 415
 Ala Val Gly Arg Ala Gln Glu Leu Met Ile Val Leu Glu Glu Tyr Ile
 420 425 430
 Arg Thr Gly Ile Ile Asp Glu Val Pro Val Tyr Ile Asp Gly Met Ile
 435 440 445
 Trp Glu Ala Asn Ala Ile His Thr Ala Arg Pro Glu Tyr Leu Ser Lys
 450 455 460
 Asp Leu Arg Asp Gln Ile Phe His Met Gly His Asn Pro Phe Ile Ser
 465 470 475 480
 Asp Ile Phe His Lys Val Asn Gly Met Asp Glu Arg Arg Glu Ile Val
 485 490 495
 Glu Gly Glu Pro Ser Ile Ile Leu Ser Thr Ser Gly Met Leu Thr Gly
 500 505 510
 Gly Asn Ser Leu Glu Tyr Phe Lys Trp Leu Cys Glu Asp Pro Asp Asn
 515 520 525
 Ser Leu Val Phe Val Gly Tyr Gln Ala Glu Gly Ser Leu Gly Arg Arg
 530 535 540
 Ile Gln Lys Gly Trp Lys Glu Ile Pro Leu Lys Asp Glu Asp Asp Lys
 545 550 555 560
 Met Arg Val Tyr Asn Val Arg Met Asn Ile Lys Thr Ile Glu Gly Phe
 565 570 575

Ser Gly His Ser Asp Arg Arg Gln Leu Met Glu Tyr Val Lys Arg Ile
 580 585 590 595

Ser Pro Lys Pro Glu Lys Ile Leu Leu Cys His Gly Asp Asn Tyr Lys
 595 600 605

Thr Leu Asp Leu Ala Ser Ser Ile Tyr Arg Thr Tyr Arg Ile Glu Thr
 610 615 620

Lys Thr Pro Leu Asn Leu Glu Thr Val Arg Ile Gln
 625 630 635

<210> 238

<211> 1040

<212> PRT

<213> Homo sapiens

<400> 238

Met Leu Glu Asp Ile Ser Glu Glu Asp Ile Trp Glu Tyr Lys Ser Lys
 1 5 10 15

Arg Lys Pro Lys Arg Val Asp Pro Asn Asn Gly Ser Lys Asn Ile Leu
 20 25 30

Lys Ser Val Glu Lys Ala Thr Asp Gly Lys Tyr Gln Ser Lys Arg Ser
 35 40 45

Arg Asn Arg Lys Arg Ala Ala Glu Ala Lys Glu Val Lys Asp His Glu
 50 55 60

Val Pro Leu Gly Asn Ala Gly Cys Gln Thr Ser Val Ala Ser Ser Gln
 65 70 75 80

Asn Ser Ser Cys Gly Asp Gly Ile Gln Gln Thr Gln Asp Lys Glu Thr
 85 90 95

Thr Pro Gly Lys Leu Cys Arg Thr Gln Lys Ser Gln His Val Ser Pro
 100 105 110

Lys Ile Arg Pro Val Tyr Asp Gly Tyr Cys Pro Asn Cys Gln Met Pro
 115 120 125

Phe Ser Ser Leu Ile Gly Gln Thr Pro Arg Trp His Val Phe Glu Cys
 130 135 140

Leu Asp Ser Pro Pro Arg Ser Glu Thr Glu Cys Pro Asp Gly Leu Leu
 145 150 155 160

Cys Thr Ser Thr Ile Pro Phe His Tyr Lys Arg Tyr Thr His Phe Leu
 165 170 175

Leu Ala Gln Ser Arg Ala Gly Asp His Pro Phe Ser Ser Pro Ser Pro
 180 185 190

Ala Ser Gly Gly Ser Phe Ser Glu Thr Lys Ser Gly Val Leu Cys Ser
 195 200 205

Leu Glu Glu Arg Trp Ser Ser Tyr Gln Asn Gln Thr Asp Asn Ser Val
 210 215 220

Ser Asn Asp Pro Leu Leu Met Thr Gln Tyr Phe Lys Lys Ser Pro Ser
 225 230 235 240

Leu Thr Glu Ala Ser Glu Lys Ile Ser Thr His Ile Gln Thr Ser Gln
 245 250 255
 Gln Ala Leu Gln Phe Thr Asp Phe Val Glu Asn Asp Lys Leu Val Gly
 260 265 270
 Val Ala Leu Arg Leu Ala Asn Asn Ser Glu His Ile Asn Leu Pro Leu
 275 280 285
 Pro Glu Asn Asp Phe Ser Asp Cys Glu Ile Ser Tyr Ser Pro Leu Gln
 290 295 300
 Ser Asp Glu Asp Thr His Asp Ile Asp Glu Lys Pro Asp Asp Ser Gln
 305 310 315 320
 Glu Gln Leu Phe Phe Thr Glu Ser Ser Lys Asp Gly Ser Leu Glu Glu
 325 330 335
 Asp Asp Asp Ser Cys Gly Phe Phe Lys Lys Arg His Gly Pro Leu Leu
 340 345 350
 Lys Asp Gln Asp Glu Ser Cys Pro Lys Val Asn Ser Phe Leu Thr Arg
 355 360 365
 Asp Lys Tyr Asp Glu Gly Leu Tyr Arg Phe Asn Ser Leu Asn Asp Leu
 370 375 380
 Ser Gln Pro Ile Ser Gln Asn Asn Glu Ser Thr Leu Pro Tyr Asp Leu
 385 390 395 400
 Ala Cys Thr Gly Gly Asp Phe Val Leu Phe Pro Pro Ala Leu Ala Gly
 405 410 415
 Lys Leu Ala Ala Ser Val His Gln Ala Thr Lys Ala Lys Pro Asp Glu
 420 425 430
 Pro Glu Phe His Ser Ala Gln Ser Asn Lys Gln Lys Gln Val Ile Glu
 435 440 445
 Glu Ser Ser Val Tyr Asn Gln Val Ser Leu Pro Leu Val Lys Ser Leu
 450 455 460
 Met Leu Lys Pro Phe Glu Ser Gln Val Glu Gly Tyr Leu Ser Ser Gln
 465 470 475 480
 Pro Thr Gln Asn Thr Ile Arg Lys Leu Ser Ser Glu Asn Leu Asn Ala
 485 490 495
 Lys Asn Asn Thr Asn Ser Ala Cys Phe Cys Arg Lys Ala Leu Glu Gly
 500 505 510
 Val Pro Val Gly Lys Ala Thr Ile Leu Asn Thr Glu Asn Leu Ser Ser
 515 520 525
 Thr Pro Ala Pro Lys Tyr Leu Lys Ile Leu Pro Ser Gly Leu Lys Tyr
 530 535 540
 Asn Ala Arg His Pro Ser Thr Lys Val Met Lys Gln Met Asp Ile Gly
 545 550 555 560
 Val Tyr Phe Gly Leu Pro Pro Lys Arg Lys Glu Glu Lys Leu Leu Gly
 565 570 575

Glu Ser Ala Leu Glu Gly Ile Asn Leu Asn Pro Val Pro Ser Pro Asn
 580 585 590
 Gln Lys Arg Ser Ser Gln Cys Lys Arg Lys Ala Glu Lys Ser Leu Ser
 595 600 605
 Asp Leu Glu Phe Asp Ala Ser Thr Leu His Glu Ser Gln Leu Ser Val
 610 615 620
 Glu Leu Ser Ser Glu Arg Ser Gln Arg Gln Lys Lys Arg Cys Arg Lys
 625 630 635 640
 Ser Asn Ser Leu Gln Glu Gly Ala Cys Gln Lys Arg Ser Asp His Leu
 645 650 655
 Ile Asn Thr Glu Ser Glu Ala Val Asn Leu Ser Lys Val Lys Val Phe
 660 665 670
 Thr Lys Ser Ala His Gly Gly Leu Gln Arg Gly Asn Lys Lys Ile Pro
 675 680 685
 Glu Ser Ser Asn Val Gly Gly Ser Arg Lys Lys Thr Cys Pro Phe Tyr
 690 695 700
 Lys Lys Ile Pro Gly Thr Gly Phe Thr Val Asp Ala Phe Gln Tyr Gly
 705 710 715 720
 Val Val Glu Gly Cys Thr Ala Tyr Phe Leu Thr His Phe His Ser Asp
 725 730 735
 His Tyr Ala Gly Leu Ser Lys His Phe Thr Phe Pro Val Tyr Cys Ser
 740 745 750
 Glu Ile Thr Gly Asn Leu Leu Lys Asn Lys Leu His Val Gln Glu Gln
 755 760 765
 Tyr Ile His Pro Leu Pro Leu Asp Thr Glu Cys Ile Val Asn Gly Val
 770 775 780
 Lys Val Val Leu Leu Asp Ala Asn His Cys Pro Gly Ala Val Met Ile
 785 790 795 800
 Leu Phe Tyr Leu Pro Asn Gly Thr Val Ile Leu His Thr Gly Asp Phe
 805 810 815
 Arg Ala Asp Pro Ser Met Glu Arg Ser Leu Leu Ala Asp Gln Lys Val
 820 825 830
 His Met Leu Tyr Leu Asp Thr Thr Tyr Cys Ser Pro Glu Tyr Thr Phe
 835 840 845
 Pro Ser Gln Gln Glu Val Ile Arg Phe Ala Ile Asn Thr Ala Phe Glu
 850 855 860
 Ala Val Thr Leu Asn Pro His Ala Leu Val Val Cys Gly Thr Tyr Ser
 865 870 875 880
 Ile Gly Lys Glu Lys Val Phe Leu Ala Ile Ala Asp Val Leu Gly Ser
 885 890 895
 Lys Val Gly Met Ser Gln Glu Lys Tyr Lys Thr Leu Gln Cys Leu Asn
 900 905 910

Val His Leu Leu Pro Met Met Gln Ile Asn Phe Lys Gly Leu Gln Ser
 930 935 940

His Leu Lys Lys Cys Gly Gly Lys Tyr Asn Gln Ile Leu Ala Phe Arg
 945 950 955 960

Pro Thr Gly Trp Thr His Ser Asn Lys Phe Thr Arg Ile Ala Asp Val
 965 970 975

Ile Pro Gln Thr Lys Gly Asn Ile Ser Ile Tyr Gly Ile Pro Tyr Ser
 980 985 990

Glu His Ser Ser Tyr Leu Glu Met Lys Arg Phe Val Gln Trp Leu Lys
 995 1000 1005

Pro Gln Lys Ile Ile Pro Thr Val Asn Val Gly Thr Trp Lys Ser Arg
 1010 1015 1020

Ser Thr Met Glu Lys Tyr Phe Arg Glu Trp Lys Leu Glu Ala Gly Tyr
 1025 1030 1035 1040

<210> 239
<211> 723
<212> PRT
<213> Arabidopsis thaliana

<400> 239
Met Ser Asn Thr Val Glu Asp Asp Asp Asp Phe Gln Ile Pro Pro
 1 5 10 15

Ser Ser Gln Leu Ser Ile Arg Lys Pro Leu His Pro Thr Asn Ala Asn
 20 25 30

Asn Ile Ser His Arg Pro Pro Asn Lys Lys Pro Arg Leu Cys Arg Tyr
 35 40 45

Pro Gly Lys Glu Asn Val Thr Pro Pro Pro Ser Pro Asp Pro Asp Leu
 50 55 60

Phe Cys Ser Ser Ser Thr Pro His Cys Ile Leu Asp Cys Ile Pro Ser
 65 70 75 80

Ser Val Asp Cys Ser Leu Gly Asp Phe Asn Gly Pro Ile Ser Ser Leu
 85 90 95

Gly Glu Glu Asp Lys Glu Asp Lys Asp Asp Cys Ile Lys Val Asn Arg
 100 105 110

Glu Gly Tyr Leu Cys Asn Ser Met Glu Ala Arg Leu Leu Lys Ser Arg
 115 120 125

Ile Cys Leu Gly Phe Asp Ser Gly Ile His Glu Asp Asp Glu Gly Phe
 130 135 140

Val Glu Ser Asn Ser Glu Leu Asp Val Leu Ile Asn Leu Cys Ser Glu
 145 150 155 160

Ser Glu Gly Arg Ser Gly Glu Phe Ser Leu Gly Lys Asp Asp Ser Ile
 165 170 175
 Gln Cys Pro Leu Cys Ser Met Asp Ile Ser Ser Leu Ser Glu Glu Gln
 180 185 190
 Arg Gln Val His Ser Asn Thr Cys Leu Asp Lys Ser Tyr Asn Gln Pro
 195 200 205
 Ser Glu Gln Asp Ser Leu Arg Lys Cys Glu Asn Leu Ser Ser Leu Ile
 210 215 220
 Lys Glu Ser Ile Asp Asp Pro Val Gln Leu Pro Gln Leu Val Thr Asp
 225 230 235 240
 Leu Ser Pro Val Leu Lys Trp Leu Arg Ser Leu Gly Leu Ala Lys Tyr
 245 250 255
 Glu Asp Val Phe Ile Arg Glu Glu Ile Asp Trp Asp Thr Leu Gln Ser
 260 265 270
 Leu Thr Glu Glu Asp Leu Leu Ser Ile Gly Ile Thr Ser Leu Gly Pro
 275 280 285
 Arg Lys Lys Ile Val Asn Ala Leu Ser Gly Val Arg Asp Pro Phe Ala
 290 295 300
 Ser Ser Ala Glu Val Gln Ala Gln Ser His Cys Thr Ser Gly His Val
 305 310 315 320
 Thr Glu Arg Gln Arg Asp Lys Ser Thr Thr Arg Lys Ala Ser Glu Pro
 325 330 335
 Lys Lys Pro Thr Ala Asn Lys Leu Ile Thr Glu Phe Phe Pro Gly Gln
 340 345 350
 Ala Thr Glu Gly Thr Lys Ile Arg Thr Ala Pro Lys Pro Val Ala Glu
 355 360 365
 Lys Ser Pro Ser Asp Ser Ser Arg Arg Ala Val Arg Arg Asn Gly
 370 375 380
 Asn Asn Gly Lys Ser Lys Val Ile Pro His Trp Asn Cys Ile Pro Gly
 385 390 395 400
 Thr Pro Phe Arg Val Asp Ala Phe Lys Tyr Leu Thr Arg Asp Cys Cys
 405 410 415
 His Trp Phe Leu Thr His Phe His Leu Asp His Tyr Gln Gly Leu Thr
 420 425 430
 Lys Ser Phe Ser His Gly Lys Ile Tyr Cys Ser Leu Val Thr Ala Lys
 435 440 445
 Leu Val Asn Met Lys Ile Gly Ile Pro Trp Glu Arg Leu Gln Val Leu
 450 455 460
 Asp Leu Gly Gln Lys Val Asn Ile Ser Gly Ile Asp Val Thr Cys Phe
 465 470 475 480
 Asp Ala Asn His Cys Pro Gly Ser Ile Met Ile Leu Phe Glu Pro Ala
 485 490 495

Asn Gly Lys Ala Val Leu His Thr Gly Asp Phe Arg Tyr Ser Glu Glu
 500 505 510
 Met Ser Asn Trp Leu Ile Gly Ser His Ile Ser Ser Leu Ile Leu Asp
 515 520 525
 Thr Thr Tyr Cys Asn Pro Gln Tyr Asp Phe Pro Lys Gln Glu Ala Val
 530 535 540
 Ile Gln Phe Val Val Glu Ala Ile Gln Ala Glu Ala Phe Asn Pro Lys
 545 550 555 560
 Thr Leu Phe Leu Ile Gly Ser Tyr Thr Ile Gly Lys Glu Arg Leu Phe
 565 570 575
 Leu Glu Val Ala Arg Val Leu Arg Glu Lys Ile Tyr Ile Asn Pro Ala
 580 585 590
 Lys Leu Lys Leu Leu Glu Cys Leu Gly Phe Ser Lys Asp Asp Ile Gln
 595 600 605
 Trp Phe Thr Val Lys Glu Glu Ser His Ile His Val Val Pro Leu
 610 615 620
 Trp Thr Leu Ala Ser Phe Lys Arg Leu Lys His Val Ala Asn Arg Tyr
 625 630 635 640
 Thr Asn Arg Tyr Ser Leu Ile Val Ala Phe Ser Pro Thr Gly Trp Thr
 645 650 655
 Ser Gly Lys Thr Lys Lys Ser Pro Gly Arg Arg Leu Gln Gln Gly
 660 665 670
 Thr Ile Ile Arg Tyr Glu Val Pro Tyr Ser Glu His Ser Ser Phe Thr
 675 680 685
 Glu Leu Lys Glu Phe Val Gln Lys Val Ser Pro Glu Val Ile Ile Pro
 690 695 700
 Ser Val Asn Asn Asp Gly Pro Asp Ser Ala Ala Ala Met Val Ser Leu
 705 710 715 720
 Leu Val Thr

<210> 240
 <211> 661
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 240
 Met Ser Arg Lys Ser Ile Val Gln Ile Arg Arg Ser Glu Val Lys Arg
 1 5 10 15
 Lys Arg Ser Ser Thr Ala Ser Ser Thr Ser Glu Gly Lys Thr Leu His
 20 25 30
 Lys Asn Thr His Thr Ser Ser Lys Arg Gln Arg Thr Leu Thr Glu Phe
 35 40 45
 Asn Ile Pro Thr Ser Ser Asn Leu Pro Val Arg Ser Ser Ser Tyr Ser
 50 55 60

Phe Ser Arg Phe Ser Cys Ser Thr Ser Asn Lys Asn Thr Glu Pro Val
 65 70 75 80
 Ile Ile Asn Asp Asp Asp His Asn Ser Ile Cys Leu Glu Asp Thr Ala
 85 90 95
 Lys Val Glu Ile Thr Ile Asp Thr Asp Glu Glu Glu Leu Val Ser Leu
 100 105 110
 His Asp Asn Glu Val Ser Ala Ile Glu Asn Arg Thr Glu Asp Arg Ile
 115 120 125
 Val Thr Glu Leu Glu Glu Gln Val Asn Val Lys Val Ser Thr Glu Val
 130 135 140
 Ile Gln Cys Pro Ile Cys Leu Glu Asn Leu Ser His Leu Glu Leu Tyr
 145 150 155 160
 Glu Arg Glu Thr His Cys Asp Thr Cys Ile Gly Ser Asp Pro Ser Asn
 165 170 175
 Met Gly Thr Pro Lys Lys Asn Ile Arg Ser Phe Ile Ser Asn Pro Ser
 180 185 190
 Ser Pro Ala Lys Thr Lys Arg Asp Ile Ala Thr Ser Lys Lys Pro Thr
 195 200 205
 Arg Val Lys Leu Val Leu Pro Ser Phe Lys Ile Ile Lys Phe Asn Asn
 210 215 220
 Gly His Glu Ile Val Val Asp Gly Phe Asn Tyr Lys Ala Ser Glu Thr
 225 230 235 240
 Ile Ser Gln Tyr Phe Leu Ser His Phe His Ser Asp His Tyr Ile Gly
 245 250 255
 Leu Lys Lys Ser Trp Asn Asn Pro Asp Glu Asn Pro Ile Lys Lys Thr
 260 265 270
 Leu Tyr Cys Ser Lys Ile Thr Ala Ile Leu Val Asn Leu Lys Phe Lys
 275 280 285
 Ile Pro Met Asp Glu Ile Gln Ile Leu Pro Met Asn Lys Arg Phe Trp
 290 295 300
 Ile Thr Asp Thr Ile Ser Val Val Thr Leu Asp Ala Asn His Cys Pro
 305 310 315 320
 Gly Ala Ile Ile Met Leu Phe Gln Glu Phe Leu Ala Asn Ser Tyr Asp
 325 330 335
 Lys Pro Ile Arg Gln Ile Leu His Thr Gly Asp Phe Arg Ser Asn Ala
 340 345 350
 Lys Met Ile Glu Thr Ile Gln Lys Trp Leu Ala Glu Thr Ala Asn Glu
 355 360 365
 Thr Ile Asp Gln Val Tyr Leu Asp Thr Thr Tyr Met Thr Met Gly Tyr
 370 375 380
 Asn Phe Pro Ser Gln His Ser Val Cys Glu Thr Val Ala Asp Phe Thr
 385 390 395 400

Leu Arg Leu Ile Lys His Gly Lys Asn Lys Thr Phe Gly Asp Ser Gln
 405 410 415
 Arg Asn Leu Phe His Phe Gln Arg Lys Lys Thr Leu Thr Thr His Arg
 420 425 430
 Tyr Arg Val Leu Phe Leu Val Gly Thr Tyr Thr Ile Gly Lys Glu Lys
 435 440 445
 Leu Ala Ile Lys Ile Cys Glu Phe Leu Lys Thr Lys Leu Phe Val Met
 450 455 460
 Pro Asn Ser Val Lys Phe Ser Met Met Leu Thr Val Leu Gln Asn Asn
 465 470 475 480
 Glu Asn Gln Asn Asp Met Trp Asp Glu Ser Leu Leu Thr Ser Asn Leu
 485 490 495
 His Glu Ser Ser Val His Leu Val Pro Ile Arg Val Leu Lys Ser Gln
 500 505 510
 Glu Thr Ile Glu Ala Tyr Leu Lys Ser Leu Lys Glu Leu Glu Thr Asp
 515 520 525
 Tyr Val Lys Asp Ile Glu Asp Val Val Gly Phe Ile Pro Thr Gly Trp
 530 535 540
 Ser His Asn Phe Gly Leu Lys Tyr Gln Lys Lys Asn Asp Asp Asp Glu
 545 550 555 560
 Asn Glu Met Ser Gly Asn Thr Glu Tyr Cys Leu Glu Leu Met Lys Asn
 565 570 575
 Asp Arg Asp Asn Asp Asp Glu Asn Gly Phe Glu Ile Ser Ser Ile Leu
 580 585 590
 Arg Gln Tyr Lys Tyr Asn Lys Phe Gln Val Phe Asn Val Pro Tyr
 595 600 605
 Ser Glu His Ser Ser Phe Asn Asp Leu Val Lys Phe Gly Cys Lys Leu
 610 615 620
 Lys Cys Ser Glu Val Ile Pro Thr Val Asn Leu Asn Asn Leu Trp Lys
 625 630 635 640
 Val Arg Tyr Met Thr Asn Trp Phe Gln Cys Trp Glu Asn Val Arg Lys
 645 650 655
 Thr Arg Ala Ala Lys
 660